

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model
Run on: July 7, 2003, 15:47:40 ; Search time 109 Seconds
(without alignments)
5122.203 Million cell updates/sec

Title: US-09-824-647-16
Perfect score: 694
Sequence: 1 cgcaggcagaccatgtgac.....ataaagtgtgtcaattttctt 2095

Scoring table:
OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 908470 seqs, 133250620 residues

Word size: 1
Total number of hits satisfying chosen parameters: 1687582

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
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-DB-A_Geneseq_101002 -OFMT=fastan -SUFFIX=std.rag -MINMATCH=0 -1-LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=45 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	593	85.4	593	20	Human GP88 autocori
2	538	77.5	593	14	Granulin sequence.
3	492	70.9	593	23	Human granulin/epi
4	410	59.1	621	21	Human cancer assoc
5	406	58.5	593	12	Human epithelin pr
6	155	22.3	413	22	Human protein sequ
7	75	10.8	77	22	Human brain expre
8	57	8.2	57	14	Granulin F. Homo
9	56	8.1	56	14	Granulin B. Homo
10	55	7.9	55	14	Granulin D. Homo
11	54	7.8	54	14	Granulin C. Homo
12	46	6.7	48	22	Human brain expre
13	34	4.9	56	14	Granulin E. Homo
14	32	4.6	54	14	Granulin G. Homo
15	32	4.6	57	23	Insulin receptor-r
16	32	4.6	57	23	Insulin receptor-r
17	32	4.6	58	23	Insulin receptor-r
18	32	4.6	58	23	Insulin receptor-r
19	32	4.6	59	23	Insulin receptor-r
20	32	4.6	58	12	Rat epithelin prec
21	32	4.6	58	12	Mouse GP88 autocori
22	32	4.6	58	20	Mouse GP88 autocori
23	32	4.6	58	23	Mouse granulin/epi
24	31	4.5	55	14	Granulin A. Homo
25	30	4.3	30	14	Paragranulin. Hom
26	19	2.7	19	20	Human GP88 autocori
27	17	2.4	51	14	Rat granulin. Rat
28	16	2.3	30	23	Human granulin A-d
29	16	2.3	30	23	Human granulin-A d
30	16	2.3	179	12	Bovine epithelin p
31	15	2.2	15	14	N-terminal amino a
32	14	2.0	14	20	Human GP88 autocori
33	11	1.6	15	13	BGP N-terminal fra
34	11	1.6	15	15	Basophil granule p
35	9	1.3	14	14	N-terminal amino a
36	8	1.2	29	21	Myobacterium tube
37	8	1.2	46	23	Rat secreted facto
38	8	1.2	56	17	Human beta 1 adren
39	8	1.2	58	23	Human ORFX protein
40	8	1.2	60	22	Human musculoskele
41	8	1.2	64	22	Propionibacterium
42	8	1.2	84	22	Novel human diagno
43	8	1.2	89	22	Human novel protei
44	8	1.2	95	22	Human nervous syst
45	8	1.2	96	22	Human novel protei

ALIGNMENTS

RESULT 1
AAW85475
ID AAW85475 standard; Protein; 593 AA.
XX
AC AAW85475;
XX
DT 15-MAR-1999 (first entry)
XX
DE Human GP88 autocrine growth factor.
XX
KW GP88; granulin; epithelin; human; growth factor; autocrine; tumour;
KW cancer; viral infection; antagonist; therapy; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 340..364
FT Peptide /note="E19V peptide used to raise antibody"
FT Peptide 566..579

/note= "A14R peptide used to raise antibody"

FT XX WO9852607-A1.
 PN XX
 PD XX 26-NOV-1998.
 XX XX 22-MAY-1998; 98WO-US10555.
 PR XX 16-DEC-1997; 97US-0991862.
 PR XX 23-MAY-1997; 97US-0863079.
 XX (SERR/) SERRERO G.
 PA XX
 PI XX Serrero G;
 XX XX
 DR XX WPI; 1999-045276/04.
 DR XX N-PSDB; ANV82825.
 XX
 PT Composition containing antagonist of growth factor GP88 - useful for
 PT treating cancer and viral diseases and also for diagnosing disease
 PT from altered GP88 expression
 PS Example 5; Fig 9A; 86pp; English.
 XX
 CC This is the amino acid sequence of human GP88, an 88 kDa
 CC glycoprotein autocrine growth factor and epithelin/granulin
 CC precursor that is expressed in a tightly regulated manner in normal
 CC cells, is overexpressed and unregulated in highly tumorigenic cells
 CC derived from normal cells, and which acts as a stringently required
 CC growth stimulator for the tumorigenic cells. Inhibition of GP88
 CC expression or action in the tumorigenic cells results in an
 CC inhibition of the tumorigenic properties of the overproducing
 CC cells. Antagonists to GP88 are used to treat diseases associated
 CC with increased expression of GP88, particularly cancer but also
 CC viral infections. Fragments of GP88 are used to raise specific
 CC antibodies (used as antagonists, as diagnostic reagents and for
 CC delivering toxins or other compounds to GP88-expressing cells) and
 CC to screen for antibodies. Methods are provided for diagnosing
 CC disease, or determining susceptibility to disease, resulting from
 CC altered GP88 activity.
 XX
 SQ Sequence 593 AA;
 Alignment Scores:
 Pred. No.: 0 Length: 593
 Score: 593.00 Matches: 593
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 85.45% Indels: 0
 DB: 20 Gaps: 0
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 QY 13 ATGTGGACCTGTGGAGCTGGTGGCTTAAACAGAGGCTGTGGTGGAAACGGGTGC 72
 Db 1 MetTprThrLeuValSerTrpValAlaLeuThralaGlyLeuValaGlyThrArgCys 20
 QY 73 CCAGATGTCAGTTCCTCCCTGTGGCTGCTGCTGGACCCCGGAGGAGCCACTACAGC 132
 Db 21 ProaspGlyGlnPheCysProValAlaCysCysLeuAspProGlyGlyAlaSerTyrSer 40
 QY 133 TGTGTCCTCCCTTCTGGAAATGGCCACACACTGACGAGGATCTGGGTGGCCCC 192
 Db 41 CysCysArgProLeuLeuAspLysTrpProThrThrLeuSerArgHisLeuGlyGlyPro 60
 QY 193 TGCAGGTGTAGTCCCACTGCTGTGGCGGCACTCTCTGCATCTTACCGTCTCAGGGACT 252
 Db 61 CysGlnValAspAlaHisCysSerAlaGlyHisSerCysTlePheThrValSerGlyThr 80
 QY 253 TCCAGTGTGTCCTTCCAGAGGCGGTGGCATGGGGATGCCCATCACTGCTGCCCA 312
 Db 81 SerSerCysCysProPheProGluAlaValaCysGlyAspGlyHisCysCysPro 100

QY 313 CGGGGCTTCCACTGCAGTGCAGCGGCGATCTCTTCCAAAGATCAGTAACTCC 372
 Db 101 ArgGlyPheHisCysSerAlaaspGlyArgSerCysPheGlnargSerGlyAsnSer 120
 QY 373 GTGGGTGCCATCCAGTGCCTGTATAGTCAATGCGAATGCCGGACTTCTCCAGTGTGT 432
 Db 121 ValGlyAlaIleGlnCysProaspSerGlnPheGluCysProaspPheSerThrCys 140
 QY 433 GTTATGTCGATGGCTCTGGGGTCTGCCCATCCAGCCCGCTCTCTGTGAAGAC 492
 Db 141 ValMetValaspGlySerTrpGlyCysCysProMetProGlnalaserCysGluasp 160
 QY 493 AGGTGTCACCTGTCTCCGACGCTGCTTCTGCGACCTGGTTCACACCCCTGCATCACA 552
 Db 161 ArgValHisCysCysProHisGlyAlaPheCysaspLeuValHisThrArgCysIleThr 180
 QY 553 CCCACGGGACCCACCCCTGGCAAGAAGACTGCTGCCAGAGGACTACACGGGCAAGT 612
 Db 181 ProThrGlyThrHisProLeuAlaLysLysLeuProAlaGlnArgThrAsnArgAlaVal 200
 QY 613 GCCTTGTCCAGCTCGCTCATGTCTCCGGAGCAGGTCCGGTCCCTGATGTTCTACC 672
 Db 201 AlaLeuSerSerSerValMetCysProaspAlaArgSerArgCysProaspGlySerThr 220
 QY 673 TGCTGTGAGCTGCCAGTGGGAAGTATGGCTGTGCCCAATGCCCAACGCCACTGTCTGC 732
 Db 221 CysCysGluLeuProSerGlyLysTyrGlyCysCysProMetProAsnAlaThrCysCys 240
 QY 733 TCCGATCAGCTGACATGGAGTGGTCCCAAGACACTGTGTGACCTGATCCAGATGAGTGC 792
 Db 241 SerAspHisLeuHisCysCysProGlnAspThrValCysaspLeuIleGlnSerLysCys 260
 QY 793 CTCTCAAGAGAGAACCTACACGACCTCTCACTAAGCTGCTGGCGACACAGTGGCG 852
 Db 261 LeuSerLysGluAsnAlaThrAspLeuLeuThrLysLeuProAlaHisThrValGly 280
 QY 853 GATGTGAATGTGACATGGAGTGGTGGTCCCAAGTGGCTATACCTGCTGCCGTCTACAG 912
 Db 281 AspValLysCysaspMetGluValSerCysProaspGlyTyrThrCysCysArgLeuGln 300
 QY 913 TCGGGGCTGGGGCTGCTGCCCTTTTACCAGGCTGTGTGCTGTGAGGACCATACAC 972
 Db 301 SerGlyAlaTrpGlyCysCysProPheThrGlnAlaValCysCysGluaspHisIleHis 320
 QY 973 TGCTGTCCCGGGTTTACGTGTGACACGACAGAGGTACCTGTGTAAACAGGGCCCCAC 1032
 Db 321 CysCysProAlaGlyPheThrCysaspThrGlnLysGlyThrCysGluGlnGlyProHis 340
 QY 1033 CAGGTGCCCTGGATGGAGAGGCCCTCAGCTCAGCTGCCAGTGGCCAGACCAAGCCTTG 1092
 Db 341 GlnValProTrpMetGluLysAlaProAlaHisLeuSerLeuProaspProGlnAlaLeu 360
 QY 1093 AAGAGAGATGTCCTCTGTGATATGTGACAGCTGTCTCTCCGATACCTGTCTGCCAA 1152
 Db 361 LysArgaspValProCysaspAsnValSerSerCysProSerSeraspThrCysGln 380
 QY 1153 CTCAGCTCTGGGAGTGGGGCTGTGTCCCAATCCAGAGGCTGTCTGCTCGGACAC 1212
 Db 381 LeuThrSerGlyGluTrpGlyCysCysProIleProGluAlaValCysCysSerAspHis 400
 QY 1213 CAGCACTGTGTCCTCCAGCATACGTGTGTAGCTGAGGGGAGTGTCTCAGCGAGGAGC 1272
 Db 401 GlnHisCysCysProGlnArgTyrThrCysValaIleGluGlyGlnCysGlnArgGlySer 420
 QY 1273 GAGATGCTGGCTGGAGAGATGCTCTGCCCGCGGGTCTCTTATCCACCCACAGA 1332
 Db 421 GluIleValaIleGlyLeuGluLysMetProAlaArgGlySerLeuSerHisProArg 440
 QY 1333 GACATCGCTGTCCACAGACACACAGCTGCCCGGTGGCGGAACCTGTCTGCCCGAGCCAG 1392
 Db 441 AspIleGlyCysaspGlnHisThrSerCysProValGlyGlyThrCysCysProSerGln 460
 QY 1393 GGTGGGAGCTGGGCTGCTGCCATGTCCTGCCCATGCTGTGTGCTGCGGAGGATGCCAGCAC 1452

|||||
Db 461 GlyCysSerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHis 480
QY 1453 TGCTGCCCGGCTGGCTACACCTGCAAGCTGGAAGCTCGATCCTCGAGAGAGAGTGGTC 1512
Db 481 CysCysProAlaGlyTyrThrCysAsnValLysAlaArgSerCysGluLysGluValVal 500
QY 1513 TCAGCCAGCTGCGCACCCTTCCTGGCCGCTAGCCCTCAGTGGGTGTGAAGGAGCTGGAG 1572
Db 501 SerAlaGlnProAlaThrPheLeuAlaArgSerProHisValGlyValLysAspValGlu 520
QY 1573 TGTGGGAAGGACACTTCTGCTGATGATACAGACCTGCTGCGCAGACACACCGACAGGGC 1632
Db 521 CysGlyGluGlyHisPheCysHisAspAsnGlnThrCysCysArgAspAsnArgGlnGly 540
QY 1633 TGGGCTGCTGCTCCCTACGCCAGGCGCTGTGTGCTGATCGCGCCCACTGCTGTCCT 1692
Db 541 TrpAlaCysCysProTyrAlaGlnGlyValCysCysAlaAspArgArgHisCysCysPro 560
QY 1693 GCTGGCTTCGCTGCGCAGCAGGGGTACCAAGTGTGTCGAGAGGAGGCGCGCTGG 1752
Db 561 AlaGlyPheArgCysAlaArgArgGlyThrLysCysLeuArgArgGluAlaProArgTrp 580
QY 1753 GACGCCCTTTGAGGGACCCAGCCTTGAGACAGCTGCTG 1791
Db 581 AspalProLeuArgAspProAlaLeuArgGlnLeuLeu 593

RESULT 2

AAR48673
ID AAR48673 standard; Protein; 593 AA.
AC AAR48673;
DT 22-APR-1994 (first entry)
DE Granulin sequence.
KW Granulin; keratinocytes; wound healing; inhibition; peptide;
KW granulocytes; leucocytes.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc-difference 452 /note= "valine encoded by ARG."
FT Misc-difference 539 /note= "glycine encoded by CAG."
PN W09315195-A.
XX
PD 05-AUG-1993.
XX
PF 28-FEB-1992; 92WO-CA00089.
XX
PR 03-FEB-1992; 92US-0829233.
XX
PA (SOLO/) SOLOMON S.
XX
PI Solomon S;
XX
DR WPI; 1993-320328/40.
XX
DR N-PSDB; AAQ49052.
XX
PT New cysteine rich granulin peptide(s) from leucocyte(s) - are
PT keratinocyte inhibitors useful topically for wound healing
XX
PS Disclosure; Figure 4c; 53pp; English.
XX
CC The granulin inhibits keratinocytes and is useful in formulations
CC for promoting the healing of wounds.
XX
SQ Sequence 593 AA;

Alignment Scores:

Pred. No.: 0 Length: 593
Score: 538.00 Matches: 538
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 77.52% Indels: 0
DB: 14 Gaps: 0

US-09-824-647-16 (1-2095) x AAR48673 (1-593)

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Db 1 MetTrpThrLeuValSerTrpValAlaLeuThrAlaGlyLeuValAlaGlyThrArgCys 20
QY 73 CCAGATGGTCAGTTCTGCCCTGTGGCTGTGGACCCCGGAGGAGCCAGCTACAGC 132
Db 21 ProAspGlyGlnPheCysProValAlaCysCysLeuAspProGlyGlyAlaSerTrpSer 40
QY 133 TGCTGCCCTGCCCTTCTGGCAAAATGGCCCAACTGAGCAGGCACTCTGGTGGCCCC 192
Db 41 CysCysArgProLeuLeuAspLysTrpProThrThrLeuSerArgHisLeuGlyGlyPro 60
QY 193 TGCAGGTTGATGCCCACTGCTGTGGCGGCCACTCTCTGCATCTTTACGCTCTCAGGACT 252
Db 61 CysGlnValAspAlaHisCysSerAlaGlyHisSerCysIlePheThrValSerGlyThr 80
QY 253 TCCAGTTGCTGCCCTTCCCAGAGGCGTGGCGGATGGCCATCAGCTGCTGCCCA 312
Db 81 SerSerCysCysProPheProGluAlaValAlaCysGlyAspGlyHisHisCysCysPro 100
QY 313 CGGGCTTCCCACTGAGTGCAGTGCAGGCGGATCTCTTCCAAAGATCAGGTAAACATCC 372
Db 101 ArgGlyPheHisCysSerAlaAspGlyArgSerCysPheGlnArgSerGlyAsnAsnSer 120
QY 373 GTGGTGCCATCCAGTGCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 432
Db 121 ValGlyAlaIleGlnCysProAspSerGlnPheGluCysProAspPheSerThrCysCys 140
QY 433 GTTATGGTGCATGGCTCTGGGGTGGTGGCGGATGGCGGATGGCGGATGGCGGATGGCG 492
Db 141 ValMetValAspGlySerTrpGlyCysCysProMetProGlnAlaSerCysCysGluAsp 160
QY 493 AGGTGTCACCTGCTGCCAGCGGTGCTTCTGCGACCTGGTTTCACACCCGCTGCATCACA 552
Db 161 ArgValHisCysCysProHisGlyAlaPheCysAspLeuValHisThrArgCysIleThr 180
QY 553 CCCAGGGCACCCACCCCTGCGAAAGAGTCCCTGCCAGAGAGACTAACAGGCGAGTG 612
Db 181 ProThrGlyThrHisProLeuAlaLysLysLeuProAlaGlnArgThrAsnArgAlaVal 200
QY 613 GCCTGTGTCAGCTCGTGCATGTGTCGGAGCAGCGTCCCGGTGCGCTGATGTTCTACC 672
Db 201 AlaLeuSerSerSerValMetCysProAspAlaArgSerArgCysProAspGlySerThr 220
QY 673 TGCTGTGAGCTGCCAGTGGGAAGTATGCTGCTGCCCAATGCCCAACGCCACCTGCTGC 732
Db 221 CysCysGluLeuProSerGlyLysTrpGlyCysCysProMetProAsnAlaThrCysCys 240
QY 733 TCCGATACCTGCTGCTGCCCGCCCAAGACACTGTGTGACCTGATGACAGTAGTAGTGC 792
Db 241 SerAspHisLeuHisCysCysProGlnAspThrValCysAspLeuIleGlnSerLysCys 260
QY 793 CTCCTCAAGGAGAACGCTACACGACGCTCCCTCACTAAGCTCCTGCGCAGCAGTGGGC 852
Db 261 LeuSerLysGluAspAlaThrThrAspLeuLeuThrLysLeuProAlaHisThrValGly 280
QY 853 GATGTGAAATGTACATGAGTGTGCTGCCAGATGGCTATACCTGCTGCCCTCTACAG 912
Db 281 AspValLysCysAspMetGluValSerCysProAspGlyTyrThrCysCysArgLeuGln 300
QY 913 TCGGGGGCTGGGGTGTGCTGCTTTTACCCAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 972
Db 301 SerGlyAlaTrpGlyCysCysProPheThrGlnAlaValCysCysGluAspHisIleHis 320

DR WPI; 2002-083093/11.
XX
XX New phase display library of variable heavy domain antigen-binding
PT fragments derived from llama antibodies, useful for in vitro selection
PT against any antigen of interest as a target
XX
XX
XX Disclosure; Page 20; 46pp; English.
XX
XX The present invention relates to a phage display library of variable
CC heavy domain (VHH or VH) fragments (sdab fragments) derived from llama
CC antibodies. The library is useful for in vitro selection against any
CC antigen of interest as a target. Single domain anti-idiotypic antibody
CC fragments are isolated from the library using phage display technology
CC and an antibody serving as an antigen. Such anti-idiotypic antibody
CC fragments have great potential in evoking the immune system response
CC to pathological antigens and in vaccine development. The large size of
CC the library considerably increases the probability of isolating from it
CC antigen-binding fragments having high affinity to almost any
CC predetermined target (antigen of interest). The library eliminates the
CC development of anti-idiotypic antibodies by immunisation and allows
CC isolation of anti-idiotypic antibodies. AAU82636-AAU82640 represent
CC peptides used in panning experiments in the present invention.
XX
XX Sequence 30 AA;
SQ
Alignment Scores:
Pred. No.: 4.49e-06 Length: 30
Score: 16.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.31% Indels: 0
DB: 23 Gaps: 0
US-09-824-647-16 (1-2095) x AAU82636 (1-30)
QY 853 GATGTGAATGTGACATGGAGTGAGTGCCTCCAGATGCTATACCTGC 900
DB 1 AspValLysCysAspMetGluValSerCysProAspGlyTyrThrCys 16
RESULT 29
AAU82638
ID AAU82638 standard; peptide; 30 AA.
XX
XX AAU82638;
XX
XX 23-APR-2002 (first entry)
XX Human granulin-A derived peptide substituted version p1781.
XX
XX Human; phage display library; variable heavy domain fragment; VHH; VH;
KW sdab fragment; single domain anti-idiotypic antibody fragment;
KW phage display technology; immune system response; CDR1/H1; CDR2; CDR3;
KW complementarity determining region; granulin-A; p1781.
XX
XX Homo sapiens.
OS
OS Synthetic.
XX
XX WO200190190-A2.
PN
PN 29-NOV-2001.
PD
XX
XX 25-MAY-2001; 2001WO-CA00763.
PF
XX
XX 26-MAY-2000; 2000US-207234P.
PR
XX
XX (CANADA) NAT RES COUNCIL CANADA.
PA
XX
XX Tanha J, Dubuc G, Narang S;
PI
XX
XX WPI; 2002-083093/11.
XX
XX New phase display library of variable heavy domain antigen-binding
PT fragments derived from llama antibodies, useful for in vitro selection

PT against any antigen of interest as a target
XX
XX Disclosure; Page 20; 46pp; English.
XX
XX The present invention relates to a phage display library of variable
CC heavy domain (VHH or VH) fragments (sdab fragments) derived from llama
CC antibodies. The library is useful for in vitro selection against any
CC antigen of interest as a target. Single domain anti-idiotypic antibody
CC fragments are isolated from the library using phage display technology
CC and an antibody serving as an antigen. Such anti-idiotypic antibody
CC fragments have great potential in evoking the immune system response
CC to pathological antigens and in vaccine development. The large size of
CC the library considerably increases the probability of isolating from it
CC antigen-binding fragments having high affinity to almost any
CC predetermined target (antigen of interest). The library eliminates the
CC development of anti-idiotypic antibodies by immunisation and allows
CC isolation of anti-idiotypic antibodies. AAU82636-AAU82640 represent
CC peptides used in panning experiments in the present invention.
XX
XX Sequence 30 AA;
SQ
Alignment Scores:
Pred. No.: 4.49e-06 Length: 30
Score: 16.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.31% Indels: 0
DB: 23 Gaps: 0
US-09-824-647-16 (1-2095) x AAU82638 (1-30)
QY 853 GATGTGAATGTGACATGGAGTGAGTGCCTCCAGATGCTATACCTGC 900
DB 1 AspValLysCysAspMetGluValSerCysProAspGlyTyrThrCys 16
RESULT 30
AAU82638
ID AAU82638 standard; Protein; 179 AA.
XX
XX AAU82638;
XX
XX 17-JAN-1992 (first entry)
XX Bovine epithelin precursor (partial).
XX
XX ET; growth regulation; inhibition; stimulation.
KW
XX
XX Bos taurus.
OS
XX
XX WO9115510-A.
PN
XX
XX 17-OCT-1991.
PD
XX
XX 03-APR-1991; 91WO-US02321.
PF
XX
XX 13-MAR-1991; 91US-0083796.
PR
XX
XX 03-APR-1990; 90US-0504508.
PR
XX
XX (BRIM) BRISTOL-MYERS SQUIB.
PA
XX
XX Shoyab M, Plowman GD;
PI
XX
XX WPI; 1991-325168/44.
DR
XX
XX N-PSDB; AAQ14952.
DR
XX
XX New cysteine-rich growth modulating proteins, epithelins - useful
PT as inhibitors of neoplastic cell growth and to promote wound
PT healing and treat psoriasis
PT
XX
XX Disclosure; Fig 24; 97pp; English.
XX
XX The epithelins appear to comprise several distinct members sharing
CC significant structural homology. Two members of the epithelin family,
CC

CC EP-1 and EP-2, have been purified from natural sources, and cDNAs
 CC encoding these and several other members of the epithelin family have
 CC been isolated from rat (AAQ14338), human (AAQ14339), bovine, murine
 CC (AAQ14340) and chicken (AAQ14953).
 CC ET-1 is a bifunctional growth regulator, capable of stimulating
 CC the growth of some cell types while inhibiting the growth of others.
 CC ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory
 CC bioactivity. In contrast, however, ET-2 is apparently not capable of
 CC eliciting the growth stimulatory activity characteristic of ET-1 and,
 CC in fact, antagonises this ET-1 activity.
 CC See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20.
 XX
 SQ Sequence 179 AA;

Alignment Scores:
 Pred. No.: 3.45e-06 Length: 179
 Score: 16.00 Matches: 16
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.31% Indels: 0
 DB: 12 Gaps: 0

US-09-824-647-16 (1-2095) x AAR15426 (1-179)

OY 892 TATACCTGCTGCGTACAGTCGGGGGCTGGGGCTGCTGCCCTTTT 939
 |||||
 DB 66 TTTTTCysCysArgLeuGlnSerGlyAlaTrpGlyCysCysProphe 81

RESULT 31

AAR35077
 ID AAR35077 standard; protein; 15 AA.

XX
 AC AAR35077;
 XX
 DT 09-AUG-1993 (first entry)
 XX
 DE N-terminal amino acid sequence of human granulin A.
 XX
 KW Transforming growth factor e; cell proliferation; mitogen.
 XX
 OS Homo sapiens.

XX
 PN WO9307173-A.
 XX
 PD 15-APR-1993.
 XX
 PF 02-OCT-1992; 92WO-US08417.
 XX
 PR 03-OCT-1991; 91US-0770585.

XX (UYGE-) UNIV GEORGIA RES FOUND INC.
 XX
 PI Halper J, McGraw RA, Parnell PG;
 XX
 DR WPI; 1993-134386/16.

XX Transforming growth factor E produced in commercial quantities -
 PT used for wound healing and burns treatment, comprises monomeric
 PT protein which acts as mitogen for fibroblasts

XX Example; Page 49; 60pp; English.

XX TGF β is a glycoprotein with an Mr of about 25,000. The partial
 CC amino acid sequence of purified bovine TGF β indicated no homology to
 CC other known growth factors. However the N-terminal sequence
 CC exhibits considerable amino acid sequence identity to the deduced N-
 CC terminal amino acid sequence of human granulin A and the N-terminus
 CC of epithelin 1.

SQ Sequence 15 AA;

Alignment Scores:
 Pred. No.: 4.48e-05 Length: 15

Score: 15.00 Matches: 15
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.16% Indels: 0
 DB: 14 Gaps: 0
 US-09-824-647-16 (1-2095) x AAR35077 (1-15)

OY 853 GARGTGAATGTCACATGAGGTGAGTCCCGACAGATGGCTATACC 897
 |||||
 DB 1 AspWallyCysAspMetGluValSerCysProAspGlyTyrThr 15

RESULT 32

AAW85481
 ID AAW85481 standard; Peptide; 14 AA.

XX
 AC AAW85481;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Human GP88 autocrine growth factor antigenic peptide A14R.

XX GP88; granulin; epithelin; human; growth factor; autocrine; tumour;
 KW cancer; viral infection; antagonist; therapy; diagnosis; antigen;
 KW antibody.

XX Homo sapiens.

XX WO9852607-A1.

XX 26-NOV-1998.

XX 22-MAY-1998; 98WO-US10555.

XX 16-DEC-1997; 97US-0991862.

XX 23-MAY-1997; 97US-0863079.

XX (SERR/) SERRERO G.

XX Serrero G;

XX WPI; 1999-045276/04.

XX Composition containing antagonist of growth factor GP88 - useful for
 PT treating cancer and viral diseases and also for diagnosing disease
 PT from altered GP88 expression

XX Example 8; Page 45; 86pp; English.

XX This is the amino acid sequence of peptide A14R, comprising amino
 CC acid residues A566-R579 of human GP88 (see AAW85475). GP88 is an 88
 CC kDa glycoprotein autocrine growth factor that is expressed in a
 CC tightly regulated manner in normal cells, is overexpressed and
 CC unregulated in highly tumorigenic cells derived from normal cells,
 CC and which acts as a stringently required growth stimulator for the
 CC tumorigenic cells. A14R was used in an attempt to raise
 CC neutralising antibodies to GP88 (see also AAW85480). Antagonists to
 CC GP88, such as anti-GP88 antibodies, are used to treat diseases
 CC associated with increased expression of GP88, particularly cancer
 CC but also viral infections. Anti-GP88 antibodies can also be used
 CC as diagnostic reagents and to deliver toxins or other compounds to
 CC GP88-expressing cells.

SQ Sequence 14 AA;

Alignment Scores:
 Pred. No.: 0.000408 Length: 14
 Score: 14.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0
 DB: 20 Gaps: 0

US-09-824-647-16 (1-2095) x AAW85481 (1-14)

OY 1708 GCACGCGGCTACCAACTGTTGGCGAGGAGGCGCGCGC 1749
 Db |||||||
 1 AlaArgGlyThrLysCysLeuArgArgGluAlaProArg 14

RESULT 33

AAR20737
 ID AAR20737 standard; Protein; 15 AA.
 AC AAR20737;
 XX
 DT 19-MAY-1992 (first entry)
 XX
 DE BGP N-terminal fraction 11.
 XX
 KW Basophil granule protein; chronic myelogenous leukemia.
 XX
 OS Homo sapiens.
 XX
 PN WO9201000-A.
 XX
 PD 23-JAN-1992.
 XX
 PF 09-JUL-1991; 91WO-US04869.
 XX
 PR 10-JUL-1990; 90US-0551263.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Scott RW, Gleich GJ, Wilde GG;
 XX
 DR WPI; 1992-056828/07.
 XX

New basophil granule proteins obtd. from cytoplasmic granules -
 for diagnosis and treatment of pathologies involving inflammatory
 and IGE-mediated responses, infection, hypersensitivity and
 leukaemia(s)

Claim 2; Page 22; 28pp; English.

A patient with a form of chronic myelogenous leukemia underwent two
 treatments of cytophoresis from which basophils were recovered.
 These were used to search for novel basophil granule proteins (BGP).
 The proteins were fractioned. Ca. 25 peaks were identified.
 Several fractions were pure enough to allow for the determination of
 a single amino acid sequence. The N-terminal sequences of eight
 such fractions are represented in AAR20736-42 and AAR22455.

SQ Sequence 15 AA;

Alignment Scores:
 Pred. NO.: 0.296 Length: 15
 Score: 11.00 Matches: 11
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.59% Indels: 0
 DB: 13 Gaps: 0

US-09-824-647-16 (1-2095) x AAR20737 (1-15)

OY 865 GACATGGAGTGAGTCCCGCAGATGGCTATACC 897
 Db |||||||
 5 AspMetGluValSerCysProAspGlyThr 15

RESULT 34

AAR51665
 ID AAR51665 standard; protein; 15 AA.
 XX
 AC AAR51665;
 XX
 DT 24-OCT-1994 (first entry)
 XX

DE Basophil granule protein N-terminal sequence.

KW Basophil granule protein; N-terminal sequence;
 KW BGP specific antibodies; Antibodies; Leukaemia.

OS Homo sapiens.

PN WO9406829-A.

XX 31-MAR-1994.

XX 10-SEP-1993; 93WO-US08511.

XX 11-SEP-1992; 92US-0943813.

PA (INCY-) INCYTE PHARM INC.

XX (MAYO-) MAYO FOUNDATION.

XX Gleich GJ, Scott RW, Wilde GG;

XX WPI; 1994-118398/14.

XX New human basophil granule proteins - and related nucleic acid,
 expression systems, antibodies, etc., for diagnosis and treatment
 of e.g. inflammation, parasitic infection, leukaemia etc.

XX Claim 2; Page 34; 55pp; English.

XX AAR51665 shows an N-terminal sequence of a basophil granule protein.
 CC The BGP can be extracted from human basophil granules by treatment
 CC at pH 9.0 or greater. This can be used to generate its corresponding
 CC nucleic acid an antibodies. Anti-BGPs are useful for the diagnosis
 CC of prepathologic conditions as well as chronic and acute diseases,
 CC such as parasitic infection and leukaemia, where there is a change
 CC in the amount or distribution of BGPs.

SQ Sequence 15 AA;

Alignment Scores:
 Pred. NO.: 0.296 Length: 15
 Score: 11.00 Matches: 11
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.59% Indels: 0
 DB: 15 Gaps: 0

US-09-824-647-16 (1-2095) x AAR51665 (1-15)

OY 865 GACATGGAGTGAGTCCCGCAGATGGCTATACC 897
 Db |||||||
 5 AspMetGluValSerCysProAspGlyThr 15

RESULT 35

AAR35078
 ID AAR35078 standard; protein; 14 AA.
 XX
 AC AAR35078;
 XX
 DT 09-AUG-1993 (first entry)
 XX
 DE N-terminal amino acid sequence of epithelin.

XX Transforming growth factor e; cell proliferation; mitogen.
 XX Homo sapiens.
 XX WO9307173-A.
 XX
 PD 15-APR-1993.
 XX
 PF 02-OCT-1992; 92WO-US08417.
 XX
 PR 03-OCT-1991; 91US-0770585.

Tue Jul 8 07:45:12 2003

XX (UTGE-) UNIV GEORGIA RES FOUND INC.
 XX Halper J, McGraw RA, Parnell PG;
 XX WPI; 1993-134386/16.
 XX Transforming growth factor E produced in commercial quantities -
 PT used for wound healing and burns treatment, comprises monomeric
 PT protein which acts as mitogen for fibroblasts
 XX Example; Page 49; 60pp; English.
 XX TGF β is a glycoprotein with an Mr of about 25,000. The partial
 CC amino acid sequence of purified bovine TGF β indicated no homology to
 CC other known growth factors. However the N-terminal sequence
 CC exhibits considerable amino acid sequence identity to the deduced N-
 CC terminal amino acid sequence of human granulosa A and the N-terminus
 CC of epithelin 1.
 XX SQ Sequence 14 AA;
 Alignment Scores:
 Pred. No.: 24.3 Length: 14
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.30% Indels: 0
 DB: 14 Gaps: 0
 US-09-824-647-16 (1-2095) x AAR35078 (1-14)
 QY 871 GAGTGAGTGGCCAGATGCTATACC 897
 Db 6 GluValSerCysProAspGlyTyrThr 14
 RESULT 36
 ABB81227
 ID ABB81227 standard; Peptide; 29 AA.
 XX ABB81227;
 AC ABB81227;
 DT 16-AUG-2002 (first entry)
 XX Mycobacterium tuberculosis PGIS peptide sequence.
 DE Mycobacterium tuberculosis; Mycobacterium bovis; Mycobacterium
 KW detection; BAC vector; bacterial artificial chromosome; tuberculosis.
 KW Mycobacterium tuberculosis.
 OS WO9954487-A2.
 XX 28-OCT-1999.
 PD 16-APR-1999; 99WO-IB00740.
 PF 16-APR-1998; 98US-0060756.
 XX (INSP) INST PASTEUR.
 XX Cole S, Buchrieser-Brosch R, Gordon S, Billault A;
 PI WPI; 2000-013262/01.
 DR Isolation of polynucleotides from mycobacterial genomes, useful for
 PT detection of Mycobacteria and for combating tuberculosis -
 XX Disclosure; Page 14; 161pp; English.
 XX The present invention describes a method for isolating a polynucleotide
 CC of interest that is present or is expressed in a genome of a first
 CC mycobacterium strain and that is absent or altered in a genome of a

CC second mycobacterium strain, which is different from the first strain
 CC using a bacterial artificial chromosome (BAC) vector. Recombinant BAC
 CC vectors, which are preferably immobilised, can be used to detect
 CC mycobacterial nucleic acids (genomic DNA, cDNA or mRNA) in biological
 CC samples. The polynucleotides identified are useful as probes or primers
 CC for detecting a given mycobacterium of interest. By aligning the
 CC polynucleotides contained in the recombinant BAC vectors it is possible
 CC to physically map a polynucleotide of mycobacterial origin in a
 CC biological sample. The methods and vectors from the present invention
 CC are useful in providing information for combating tuberculosis. It is
 CC possible to compare genomes between different strains or species and
 CC their non-pathogenic strains or species counterparts. ABO62492 to
 CC ABO63228 and ABB81227 to ABB81230 represent sequences used in the
 CC exemplification of the present invention.
 XX SQ Sequence 29 AA;
 Alignment Scores:
 Pred. No.: 197 Length: 29
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.16% Indels: 0
 DB: 21 Gaps: 0
 US-09-824-647-16 (1-2095) x ABB81227 (1-29)
 QY 1231 GCTGGGGCAGCAGTCTGTGGT 1208
 Db 6 AlaGlyGlySerAlaGlyGly 13
 RESULT 37
 AAU70166
 ID AAU70166 standard; Protein; 46 AA.
 XX AAU70166;
 AC AAU70166;
 XX 12-MAR-2002 (first entry)
 DT Rat secreted factor protein encoded by DNA clone P0239_C11.
 XX Rat; secreted factor polypeptide; cardiac disease; renal disease; kidney;
 KW inflammatory disease; congestive heart failure; myocarditis; asthma;
 KW dilated congestive cardiomyopathy; angina pectoris; cardiac arrhythmia;
 KW myocardial infarction; pulmonary hypertension; arteriosclerosis; stroke;
 KW atherosclerosis; cardiac tumour; glomerulonephritis; nephrotic syndrome;
 KW renal infarction; hereditary nephritis; polycystic kidney disease;
 KW chronic renal failure; renal vein thrombosis; medullary sponge kidney;
 KW rheumatoid arthritis; osteoarthritis; psoriasis; restenosis;
 KW graft versus host reaction; Crohn's disease; ulcerative colitis;
 KW Alzheimer's disease; gene therapy.
 XX Rattus norvegicus.
 OS WO200174901-A2.
 XX 11-OCT-2001.
 PD 23-MAR-2001; 2001WO-US09555.
 XX 31-MAR-2000; 2000US-193548P.
 PR 14-MAR-2001; 2001US-080954S.
 XX (SCIO-) SCIOS INC.
 XX Stanton LW, White RT;
 PI WPI; 2002-010779/01.
 DR N-PSDB; AAS94714.
 XX Novel secreted factor polypeptide useful for treating cardiac diseases
 PT such as arteriosclerosis, myocardial infarction, inflammatory diseases
 PT such as asthma, stroke, and rheumatoid arthritis and renal diseases

XX Claim 18; Fig 22; 189pp; English.
PS
XX The invention relates to rat secreted factor polypeptides and the
XX polynucleotides encoding them. The sequences are useful for treating
CC cardiac, renal or inflammatory diseases. These include cardiac diseases
CC such as congestive heart failure, myocarditis, dilated congestive
CC cardiomyopathy, angina pectoris, myocardial infarction, cardiac
CC arrhythmia, pulmonary hypertension, arteriosclerosis, atherosclerosis and
CC cardiac tumours, renal diseases such as glomerulonephritis, nephrotic
CC syndrome, renal infarction, hereditary nephritis, polycystic kidney
CC disease, chronic renal failure, renal vein thrombosis and medullary
CC sponge kidney and inflammatory diseases such as asthma, rheumatoid
CC arthritis, osteoarthritis, stroke, psoriasis, restenosis, graft versus
CC host reaction, Crohn's disease, ulcerative colitis and Alzheimer's
CC disease. Sequences AAU70146-AAU70178 represent the secreted factor
CC polypeptides of the invention.
XX
SQ Sequence 46 AA;

Alignment Scores:
Pred. No.: 184 Length: 46
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 23 Gaps: 0

US-09-824-647-16 (1-2095) x AAU70166 (1-46)

QY 494 CTGCTTTCACAGCAGGACCTGG 471
DB 25 LeuSerSerGlnGlnGluAlaTrp 32

RESULT 38

AAW03586
ID AAW03586 standard; peptide; 56 AA.

XX
AC AAW03586;

XX 17-DEC-1996 (first entry)

XX Human beta 1 adrenergic #1 GPR N-terminal sequence.

XX G-protein coupled receptor; ligand binding assay; transmembrane domain;
KW schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin;
KW muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;
KW odorant; cytomegalovirus; serotonergic.
XX
OS Homo sapiens.

XX US5508384-A.

XX 16-APR-1996.

XX 10-SEP-1992; 92US-0943236.

XX 09-SEP-1993; 93US-0118270.

XX 10-SEP-1992; 92US-0943236.

XX (UUNY) UNIV NEW YORK STATE.

XX Murphy RB, Schuster DI;

XX WPI; 1996-208785/21.

XX New dopamine receptor peptide - useful as antipsychotic agent, e.g.
PT for treating schizophrenia
XX
XX Disclosure; Fig 8B(1); 184pp; English.

XX Proteins AAW02657-W02720 represent a range of G-protein coupled receptor
CC (GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine,

CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
CC odorant, cytomegalovirus and other GPR proteins. The peptides
CC AAW03578-W03651 represent the N-terminal fragments of the above
CC proteins. The receptor proteins were used to design polypeptides, pref.
CC based on the transmembrane domains, for use in G-protein coupled receptor
CC ligand binding assays. The polypeptide fragments retain biological
CC activity such as binding a GPR ligand or modulating GPR ligand binding to
CC a GPR (see AAW02747-W02999 for examples of polypeptide fragments).
CC The polypeptide fragments can be used in compositions for treating
CC subjects suffering from a pathology related to a GPR abnormality e.g. a
CC psychotic disorder such as schizophrenia.

XX Sequence 56 AA;

Alignment Scores:
Pred. No.: 179 Length: 56
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 17 Gaps: 0

US-09-824-647-16 (1-2095) x AAW03586 (1-56)

QY 1209 CCACCAGCAGCTGCTGCCGCCGCG 1232
DB 38 ProProAlaLeuLeuProAla 45

RESULT 39

ABP04295

ID ABP04295 standard; Protein; 58 AA.

XX AC ABP04295;

XX 24-JUN-2002 (first entry)

XX Human ORFX protein sequence SEQ ID NO:8572.

XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;
KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myasthenia gravis.

XX OS Homo sapiens.

XX WO200192523-A2.

XX 06-DEC-2001.

XX 29-MAY-2001; 2001WO-US10836.

XX 30-MAY-2000; 2000US-206132P.

XX 29-AUG-2000; 2000US-228716P.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach MD;

XX WPI; 2002-106308/14.

XX N-PSDB; ABN20047.

XX Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and autoimmune disorders

XX Disclosure; SEQ ID 8572; 1037pp; English.

XX The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1

CC in the specification). ABN15762 to ABN27252 encode the human ORFX
 CC proteins given in ABP0010 to ABP11500. ORFX proteins are useful for
 CC treating or preventing a pathology associated with an ORFX-associated
 CC disorder in humans, and in the manufacture of a medicament for treating a
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
 CC sequences can be used in gene therapy. ORFX sequences can be used in the
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
 CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, infectious
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC bone degenerative disorders, or periodontal disease, and for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues and conditions resulting from
 CC systemic cytokine damage.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 58 AA;

Alignment Scores:
 Pred. No.: 178 Length: 58
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.15% Indels: 0
 DB: 23 Gaps: 0

US-09-824-647-16 (1-2095) x ABP04295 (1-58)

QY 1428 TGTGTGTCGGAGGATCGCAGCA 1451
 |||||
 Db 42 CysValleuArgGlySerProAla 49

RESULT 40

ABB03646

ID ABB03646 standard; Protein; 60 AA.

XX AC ABB03646;

XX DT 08-JAN-2002 (first entry)

XX XX Human musculoskeletal system related polypeptide SEQ ID NO 1593.

DE Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antilucer;
 KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein;
 KW musculoskeletal system.

OS Homo sapiens.

XX XX WO20015367-A1.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01338.

XX XX 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226868.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.

PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 01-NOV-2000; 2000US-0244674.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX
PA (HUNA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX
XX WPI; 2001-451937/48.
DR N-PSDB; AAL35228.
XX
XX
XX Isolated polypeptide for treating, preventing and/or prognosing
PT disorders related to the musculoskeletal system including
PT musculoskeletal cancers and also for testing and detection e.g.
PT diagnosis -
XX
XX
PS Claim 11; SEQ ID NO 1593; 781pp + Sequence Listing; English.

XX The invention relates to novel genes (AAL34669-AAL37666) and proteins
CC (ABB03087-ABB04109) associated with the musculoskeletal system useful
CC for preventing, treating or ameliorating medical conditions e.g. by

CC protein or gene therapy. The genes are isolated from a range of human
CC tissues disclosed in the specification. The nucleic acids, proteins,
CC antibodies and (ant)agonists are useful in the diagnosis, treatment,
CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and
CC gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound
CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
CC and (f) infectious diseases such as viral, bacterial, fungal and
CC parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 60 AA;

Alignment Scores: 177 Length: 60
Pred. No.: 8.00 Matches: 8
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 1.15% Indels: 0
Query Match: 22 Gaps: 0
DB:

US-09-824-647-16 (1-2095) x ABB03646 (1-60)

QY 1022 AGGGCCCCCACCAGTGCCTGGA.1045

DB 3 ArgGlyProThrArgCysProGly 10

RESULT 41

AAU42545

ID AAU42545 standard; Protein; 64 AA.

AC AAU42545;

DT 27-FEB-2002 (first entry)

DE Propionibacterium acnes immunogenic protein #3441.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.

OS Propionibacterium acnes.

PN WO200181581-A2.

PD 01-NOV-2001.

PF 20-APR-2001; 2001WO-US12865.

PR 21-APR-2000; 2000US-199047P.

PR 02-JUN-2000; 2000US-208841P.

PR 07-JUL-2000; 2000US-216747P.

XX (CORI-) CORIXA CORP.

XX Skelky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX WPI; 2001-616774/71.

DR N-PSDB; AAS59517.

XX Propionibacterium acnes polypeptides and nucleic acids useful for

PT vaccinating against and diagnosing infections, especially useful for

PT treating acne vulgaris -

XX Example 1; SEQ ID No 3740; 1069pp; English.

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 64 AA;

Alignment Scores:
 Pred. No.: 176 Length: 64
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.16% Indels: 0
 DB: 22 Gaps: 0

US-09-824-647-16 (1-2095) x AAU42545 (1-64)

Qy 1317 GGACCGCGCGGCGAGGCATCTT 1294
 Db 43 GlyThrAlaAlaGlyArgHisLeu 50
 |||||

RESULT 42

ABG03704
 ID ABG03704 standard; Protein: 84 AA.

XX ABG03704;

XX 13-FEB-2002 (first entry)

XX Novel human diagnostic protein #3695.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS67891.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity

XX Claim 20; SEQ ID-No 34063; 103pp; English.
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 84 AA;

Alignment Scores:
 Pred. No.: 169 Length: 84
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.15% Indels: 0
 DB: 22 Gaps: 0

US-09-824-647-16 (1-2095) x ABG03704 (1-84)

Qy 288 CGGGATGGCCATCAGTCGTCGCC 311
 Db 20 ArgGlyTrpProSerLeuLeuPro 27
 |||||

RESULT 43

AAU14455

ID AAU14455 standard; Protein: 89 AA.

XX AAU14455;

XX 24-OCT-2001 (first entry)

XX Human novel protein #326.

XX Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
 KW immunomodulatory; cytostatic; neuroprotective; vulnery; nootropic;
 KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
 KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
 KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
 KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
 KW tissue regeneration; immune disorder.

XX Homo sapiens.

XX WO200155437-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02623.

XX 25-JAN-2000; 2000US-0491404.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 02-OCT-2000; 2000US-0237041.
PR 13-OCT-2000; 2000US-0239335.
PR 13-OCT-2000; 2000US-0239337.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0242221.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249219.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0251160.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 08-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-541565/60.
XX N-PSDB; ABA13756.
DR

XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system
PT cancers and metastases -
XX
PS Claim 11; SEQ ID NO 6087; 1701pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABA11004-ABA21534) and proteins
CC (ABA14678-ABA18001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 95 AA;

Alignment Scores:
Pred. No.: 166 Length: 95
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 22 Gaps: 0

US-09-824-647-16 (1-2095) x ABB17430 (1-95)
QY 1896 CCCATTCTGAGTCCCAATCACCA 1919
Db 12 ProileuSerSerProSerPro 19
|||||
RESULT 45
AAU14219
ID AAU14219 standard; Protein; 96 AA.
XX AAU14219;
AC AAU14219;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human novel protein #90.
XX
KW Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.
XX
OS Homo sapiens.
XX
XX WO200155437-A2.
PN
XX
PD 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-US02623.
XX
XX 25-JAN-2000; 2000US-0491404.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
PI

```
XX WPI; 2001-451939/48.
DR N-PSDB; AAS22524.
XX
PT Isolated polypeptides useful for treating anti-inflammatory diseases,
XX nervous system disorders, and for regenerating bone and cartilage -
XX
XX Example 4; Page 572; 894pp; English.
XX
XX The invention relates to polynucleotides encoding novel human
XX proteins or their active domains. The polypeptides, polynucleotides and
XX antibodies raised against the polypeptides are used in a method of
XX treatment of a mammal and prevention of disorders caused by the aberrant
XX protein expression or activity. The polypeptides can be used as
XX molecular weight markers, food supplements, and in antibody production.
XX The polypeptides are used to identify compounds which bind to the
XX polypeptides. Polynucleotides of the invention are used as probes and
XX primers, for sequencing, for chromosome or gene mapping, in the
XX production of recombinant proteins, and in generating anti-sense DNA or
XX RNA and in gene therapy. Polypeptides of the invention can be used to
XX target drugs to a tumour, in assays to determine biological activity, to
XX raise antibodies/elicit an immune response, to determine quantitative
XX protein levels, as tissue markers, and to isolate receptors or ligands.
XX Polypeptides of the invention may also be useful in treating platelet
XX disorders, stem cell disorders, regenerating bone, cartilage, tendon,
XX ligament and/or nerve tissue, wound healing, treating burns, promoting
XX the proliferation, differentiation and survival of stem cells, as a
XX contraceptive, treating osteoporosis and osteoarthritis, anaemia,
XX Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
XX sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
XX fungal infection or from autoimmunity, cancer, allergy, asthma,
XX graft-versus-host disease, eczema, haemophilia, thrombosis,
XX anti-inflammatory diseases, nervous system disorders, and infection.
XX The present sequence represents a protein of the invention.
XX
SQ Sequence 96 AA;

Alignment Scores:
Pred. No.: 165 Length: 96
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 22 Gaps: 0

US-09-824-647-16 (1-2095) x AAU14219 (1-96)
QY 1511 TCCTGCCCCAGCCGCGACCTTC 1534
DB 57 SerLeuProSerLeuProSer 64

Search completed: July 7, 2003, 15:55:14
Job time : 140 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: July 7, 2003, 15:49:17 ; Search time 77 Seconds
(without alignments)
6257.407 Million cell updates/sec

Title: US-09-824-647-16

Perfect score: 694

Sequence: 1 cgcaggcagaccatgtgac.....ataaagttgtcaactttctt 2095

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 440863 seqs, 114992915 residues

Word size: 1

Total number of hits satisfying chosen parameters: 826674

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-DB=PublishedApplications_AA -OFMT=fastan -SUFFIX=std.rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=45 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USFR=US09824647.cgn_1_1_24_brunat_07072003_154720_26102
-NCPU=6 -ICPU=3 -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-Fgapop=6 -Fgapext=7 -Ygapop=60 -Ygapext=60 -DELOP=6 -DELEXT=7

Database :

Published Applications_AA:

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pcp.*
2: /cgn2_6/ptodata/1/pubpaa/PT_NEW_PUB.pcp.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pcp.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pcp.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pcp.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
7: /cgn2_6/ptodata/1/pubpaa/PTUS_PUBCOMB.pcp.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
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10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pcp.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pcp.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pcp.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	593	85.4	593	9	US-09-824-647-17
2	593	85.4	593	9	US-10-218-509-17
3	593	85.4	593	9	US-10-281-160-17
4	593	85.4	593	10	US-09-813-156-17

5	593	85.4	593	10	US-09-824-807-17	Sequence 17, Appl
6	410	59.1	621	10	US-09-925-301-1416	Sequence 1416, Ap
7	75	10.8	77	10	US-09-864-761-43653	Sequence 43653, A
c	46	6.7	48	10	US-09-864-761-43654	Sequence 43654, A
9	32	4.6	57	9	US-09-874-056-4	Sequence 4, Appl
10	32	4.6	58	9	US-09-874-056-5	Sequence 5, Appl
11	32	4.6	58	9	US-09-874-056-7	Sequence 7, Appl
12	32	4.6	589	9	US-09-824-647-2	Sequence 2, Appl
13	32	4.6	589	9	US-10-218-509-2	Sequence 2, Appl
14	32	4.6	589	9	US-10-281-160-2	Sequence 2, Appl
15	32	4.6	589	10	US-09-813-156-2	Sequence 2, Appl
16	32	4.6	589	10	US-09-824-807-2	Sequence 2, Appl
17	19	2.7	19	9	US-09-824-647-6	Sequence 6, Appl
18	19	2.7	19	9	US-10-218-509-6	Sequence 6, Appl
19	19	2.7	19	9	US-10-281-160-6	Sequence 6, Appl
20	19	2.7	19	10	US-09-813-156-6	Sequence 6, Appl
21	19	2.7	19	10	US-09-824-807-6	Sequence 6, Appl
22	17	2.4	57	9	US-09-874-056-3	Sequence 3, Appl
23	16	2.3	59	9	US-09-874-056-6	Sequence 6, Appl
24	14	2.0	14	9	US-09-824-647-7	Sequence 7, Appl
25	14	2.0	14	9	US-10-218-509-7	Sequence 7, Appl
26	14	2.0	14	9	US-10-281-160-7	Sequence 7, Appl
27	14	2.0	14	10	US-09-813-156-7	Sequence 7, Appl
28	14	2.0	14	10	US-09-824-807-7	Sequence 7, Appl
c	29	8	46	10	US-09-809-545A-43	Sequence 43, Appl
30	8	1.2	60	10	US-09-764-877-1593	Sequence 1593, Ap
31	8	1.2	97	9	US-10-039-836A-2	Sequence 2, Appl
32	8	1.2	109	10	US-09-925-301-1558	Sequence 1558, Ap
33	8	1.2	151	10	US-09-934-465-11	Sequence 11, Appl
34	8	1.2	166	9	US-10-237-271-18	Sequence 18, Appl
35	8	1.2	190	9	US-10-156-761-12579	Sequence 12579, A
36	8	1.2	192	9	US-10-245-103-48	Sequence 48, Appl
37	8	1.2	192	9	US-10-245-107-48	Sequence 48, Appl
38	8	1.2	192	9	US-10-245-143-48	Sequence 48, Appl
39	8	1.2	192	9	US-10-245-771-48	Sequence 48, Appl
40	8	1.2	192	9	US-10-245-851-48	Sequence 48, Appl
41	8	1.2	192	9	US-10-245-883-48	Sequence 48, Appl
42	8	1.2	192	9	US-10-237-533-48	Sequence 48, Appl
43	8	1.2	192	9	US-10-238-183-48	Sequence 48, Appl
44	8	1.2	192	9	US-10-238-283-48	Sequence 48, Appl
45	8	1.2	192	9	US-10-238-370-48	Sequence 48, Appl

ALIGNMENTS

RESULT 1
US-09-824-647-17
; Sequence 17, Application US/09824647
; Publication No. US20020183270A1
; GENERAL INFORMATION:
; APPLICANT: Serrero, Glnette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996.488/P001-A
; CURRENT APPLICATION NUMBER: US/09/824,647
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,862
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 17
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Human GP88 cDNA
US-09-824-647-17

Alignment Scores:
Pred. No.: 0
Score: 593.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 85.45%
Length: 593
Matches: 593
Conservative: 0
Mismatch: 0
Indels: 0

RESULT 2
US-10-218-509-17
; Sequence 17, Application US/10218509
; Publication No. US20030092661A1
; GENERAL INFORMATION:
; APPLICANT: Seriero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996.488/P001-A
; CURRENT APPLICATION NUMBER: US/10/218,509
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 08/991,862
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Human GP88 CDNA
US-10-218-509-17

221	CysCysGluLeuProSerGlyLysTyrrGlyCysCysProMetProAsnAlaThrCysCys	240
733	TCCGATCACTGCCTGCTGCCCCAGACACAGCTGTGTGCTACCTGATCCAGAGTAAGTC	792
241	SerAspHisLeuHisCysCysProGlnAspThrValCysAspLeulleGlnSerLysCys	260
793	CTCTCCAAAGGAAACGCTTACCACGGACCTCCTCACTAAGCTGCTGGCACACAGTGGCC	852
261	LeuSerLysGluAsnAlaThrThrAspLeuLeuThrLysLeuProAlaHisThrValGly	280
853	GATCTGAATGTGATCATGGAGGTGAGCTGCCACATGGCTATACCTGCTGCCCTCACAG	912
281	AspValLysCysAspMetGluValSerCysProaspGlyThrThrCysCysArgLeuGln	300
913	TCGGGGGCGCTGGGGGTGTGCCCTTTTACCAGCGCTGTGTGCTGTGAGGACCACATACAC	972
301	SerGlyAlaThrPglYcysCysProPheThrGlnAlaValCysCysGluAspHisIleHis	320
973	TGCTGTCCCGGGGGTTTACGTGTGCACACGACGAAGGTACCTGTGAACAGGGGGCCCCAC	1032
321	CysCysProAlaIleGlyPheThrCysaspThrGlnLysGlyThrCysGluGlnGlyProHis	340

Alignment Scores:

Pred. No.: 0 0 Length: 593
 Score: 593.00 Matches: 593
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 85.45% Indels: 0
 DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-10-218-509-17 (1-593)

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Qy 13 ATGTGGACCTGTGTGAGCTGGTGGCTTAACACAGGCTGTGTGCTGGAACGCGTGC 72
Db 1 MetTrpThrLeuValSerTrpValAlaLeuThrAlaGlyLeuValAlaGlyThrArgCys 20
Qy 73 CCAGATGGTCAGTCTCCCTGTGGCTGTGCTGGACCCCGGAGAGCCAGCTACAGC 132
Db 21 ProAspGlyGlnPheCysProValAlaCysCysLeuAspProGlyGlyAlaSerTyrSer 40
Qy 133 TGCTGGCGTCCCTTCTGGCAATGGCCACACACTGACAGGATCTGGGTGGCCCC 192
Db 41 CysCysArgProLeuLeuAspLysTrpProThrThrLeuSerArgHisLeuGlyGlyPro 60
Qy 193 TGGCAGGTGATGCCACTGTCTGCGGGCCACTCCCTGCATCTTTACGCTCTCAGGACT 252
Db 61 CysGlnValAspAlaHisCysSerAlaGlyHisSerCysIlePheThrValSerGlyThr 80
Qy 253 TCCAGTGTGCTCCCTTCCAGAGCGCGTGCATGCGGGGATGCCATCATCTGCTGCCCA 312
Db 81 SerSerCysCysProPheProGluAlaValAlaCysGlyAspGlyHisLeCysCysPro 100
Qy 313 CGGGCTTCCACTCAGTCAGAGCGGGGATCCCTGCTTCCAAAGATCAGGTAAACATCC 372
Db 101 ArgGlyPheHisCysSerAlaAspGlyArgSerCysPheGlnArgSerGlyAsnSer 120
Qy 373 GTGGTGCCATCCACTGCTGATAGTCAGTTCGAATGCCGGGACTTCTCCACCTGTGT 432
Db 121 ValGlyAlaIleGlnCysProAspSerGlnPheGluCysProAspPheSerThrCysCys 140
Qy 433 GTTATGTGATGCTCTGCGGCTGTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCT 492
Db 141 ValMetValAspGlySerTrpGlyCysCysProMetProGlnAlaSerCysCysGluAsp 160
Qy 493 AGGTGTCACTCTCTGCGACGGTCTTCTGCGACCTGTTTACACCCGCTGCATCACA 552
Db 161 ArgValHisCysCysProHisGlyAlaPheCysAspLeuValHisThrArgCysIleThr 180
Qy 553 CCCAGGCGACCCACCCCTGCAAGAAGCTCCCTGCCAGAGGACTTAACAGGCGCAGTG 612
Db 181 ProThrGlyThrHisProLeuAlaLysLysLeuProAlaGlnArgThrAsnArgAlaVal 200
Qy 613 GCCTGTGCCAGCTCGGTATGTGCGGACGACGGTCCCGGTGCTGATGGTTCACAC 672
Db 201 AlaLeuSerSerValMetCysProAspAlaArgSerArgCysProAspGlySerThr 220
Qy 673 TGCTGTGAGTCCAGTGGGAGTATGGTGTGCTGCCCAATGCCCAACGCGCCACTGTGC 732
Db 221 CysCysGluLeuProSerGlyLysTyrGlyCysCysProMetProAsnAlaThrCysCys 240
Qy 733 TCCGATCACCTGCTGCTGCCCAAGACACTGTGTGACCTGATCCAGTAAAGTGC 792
Db 241 SerAspHisLeuHisCysCysProGlnAspThrValCysAspIleGlnSerLysCys 260
Qy 793 CTCTCCAGGAGACGCTACACGACCTCTCTACTAAGCTGCTGCGCACACAGTGGGC 852
Db 261 LeuSerLysGluAsnAlaThrThrAspLeuLeuThrLysLeuProAlaHisThrValGly 280
Qy 853 GATGTGAATGTGATGGAGTGTGAGTGTGCGGATGGCTATACCTGCTGCTGCTACAG 912
Db 281 AspValLysCysAspMetGluValSerCysProAspGlyTyrThrCysCysArgLeuGln 300
Qy 913 TCGGGGCTGGGCTGCTGCTGCTTTTACCCAGGCTGTGCTGTGAGGACCATACAC 972
Db 301 SerGlyAlaTrpGlyCysCysProPheThrGlnAlaValCysCysGluAspHisIleHis 320

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Qy 973 TGCTGTCCCGGGGGTTTACGTGTGACACGAGAGGTACTCTGTGAACGGGCCCCAC 1032
Db 321 CysCysProAlaGlyPheThrCysAspThrGlnLysGlyThrCysGluGlnGlyProHis 340
Qy 1033 CAGTGTCCCTGGATGGAGAGGCCACAGTCCAGCTGAGCTGCGAGAGCCACACAGCCTTG 1092
Db 341 GlnValProTrpMetGluLysAlaProAlaHisLeuSerLeuProAspProGlnAlaLeu 360
Qy 1093 AAGAGAGATGTCCCTGTGATAATGTGACGAGCTGTCCCTCTCCGATACCTGTGCCAA 1152
Db 361 LysArgAspValProCysAspAsnValSerSerCysProSerSerAspThrCysCysGln 380
Qy 1153 CTACAGTCTGGGAGTGGGCTGTCTCCAAATCCAGAGGTGTCTGTCTGCTGCGACAC 1212
Db 381 LeuThrSerGlyGluTrpGlyCysCysProIleProGluAlaValCysCysSerAspHis 400
Qy 1213 CAGCACTGCTCCCGCCAGCGATACAGTGTGCTGAGGGGAGTGTGACGAGGAGC 1272
Db 401 GlnHisCysCysProGlnArgTyrThrCysValAlaGluGlyGlnCysGlnArgGlySer 420
Qy 1273 GAGATCTGTGGTGGACTGGAGAGATGCTGCCCGCGCGTCTCTTATCCACCCAGAG 1332
Db 421 GluIleValAlaGlyLeuGluLysMetProAlaArgArgGlySerLeuSerHisProArg 440
Qy 1333 GACATCGGCTGTGACACACACAGTGGCCCGGCTGGGCGGAACCTGCTGCCCGAGCAG 1392
Db 441 AspIleGlyCysAspGlnHisThrSerCysProValGlyThrCysCysProSerGln 460
Qy 1393 GGTGGAGCTGGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1452
Db 461 GlyGlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHis 480
Qy 1453 TGCTGCCCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1512
Db 481 CysCysProAlaGlyTyrThrCysAsnValLysAlaArgSerCysGluLysGluValVal 500
Qy 1513 TCTGCCAGCTGCCACCTTCTGCGCGGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1572
Db 501 SerAlaGlnProAlaThrPheLeuAlaArgSerProHisValGlyValLysAspValGlu 520
Qy 1573 TGTGGGAAGACACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1632
Db 521 CysGlyGluGlyHisPheCysHisAspAsnGlnThrCysCysArgAspArgHisCysCysPro 540
Qy 1633 TGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1692
Db 541 TrpAlaCysCysProTyrAlaGlnGlyValCysCysAlaAspArgArgHisCysCysPro 560
Qy 1693 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1752
Db 561 AlaGlyPheArgCysAlaArgGlyThrLysCysLeuArgGluAlaProArgTrp 580
Qy 1753 GACCCCTTTGAGGAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1791
Db 581 AspaProLeuArgAspProAlaLeuArgGlnLeuLeu 593

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RESULT 3

US-10-281-160-17
 ; Sequence 17, Application US/10281160
 ; Publication No. US20030108950A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sertero, Ginette
 ; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
 ; FILE REFERENCE: 29996.488/P001-A
 ; CURRENT APPLICATION NUMBER: US/10/281,160
 ; PRIOR FILING DATE: 2002-10-28
 ; PRIOR APPLICATION NUMBER: US/08/991,862
 ; PRIOR FILING DATE: 1998-08-17
 ; PRIOR APPLICATION NUMBER: 08/863,862
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: Patentin Ver. 2.0

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US-09-813-156-17
; Sequence 17, Application US/09813156
; Patent No. US20020061859A1
; GENERAL INFORMATION:
; APPLICANT: Scriero, Ginette
; TITLE OF INVENTION: 88 KDa TUMORIGEN
; FILE REFERENCE: Z9996.488/P001-A
; CURRENT APPLICATION NUMBER: US/09/8
; CURRENT FILING DATE: 2001-03-21

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; PRIOR APPLICATION NUMBER: 08/991,862
 ; PRIOR FILING DATE: 1997-12-16
 ; PRIOR APPLICATION NUMBER: 08/863,862
 ; PRIOR FILING DATE: 1997-05-23
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO. 17
 ; LENGTH: 593
 ; TYPE: prt
 ; ORGANISM: Human GP88 CDNA
 ; US-09-813-156-17

Alignment Scores:	
Pred. No.:	0
Score:	533.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	85.45%
DB:	10
Length:	593
Matches:	593
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-824-647-16 (1-2095) x US-09-813-156-17 (1-593)

QY	13	ANGTGGACCCCTGGGTGAGCTGGGTGGCCCTTAACAGCAGGGCTGTGGCTGGAGCCGGTGC	72
Db	1	MettrpThrLeuValSerTrpValAlaLeuThrAlaGlyLeuValAlaGlyThrArgCys	20
QY	73	CCAGATGTCAGTTCTGCCCTGCTGGCTGGACCCCGAGAGACCCAGCTACACG	132
Db	21	ProAspGlyGlnPheCysProValAlaCysCysLeuaspProGlyAlaSerTyrSer	40
QY	133	TGCTGCCGTCCTCCCTTCTGCACAAATGGCCACACACTGACGAGGANTCTGGGTGCCCC	192
Db	41	CysCysArgProLeuLeuAspLysTrpProThrThrLeuSerArgHisLeuGlyGlyPro	60
QY	193	TGCCAGGTGTGATGCCCACTGCTCTGCGCGCCACCTCTGCATCTTTACCGTCTCAGGACT	252
Db	61	CysGlnValAspAlaHisCysSerAlaGlyHisSerCysTlePheThrValSerGlyThr	80
QY	253	TCCAGTTGCTGCCCTTCCCAGAGCCGTGGCATGCCGGATGGCCATCACTGCTGCCCA	312
Db	81	SerSerCysCysProPheProGluAlaValAlaCysGlyAspGlyHisHisCysCysPro	100
QY	313	CGGGCTTCCACTGCAGTCGACAGCGGGCGATCCCTGCTTCCAAAGATCAGGTAAACA	372
Db	101	ArgGlyPheHisCysSerAlaAspGlyArgSerCysPheGlnArgSerGlyAsnSer	120
QY	373	GTGGGTGCCATCCAGTGCCTGTATGACGTTCGAATGCCCGGAGCTTCTCCAGTCTGT	432
Db	121	ValGlyAlaIleGlnCysProAspSerGlnPheGluCysProAspPheSerThrCysCys	140
QY	433	GTTATGGTCGATGCTCTCGGGGTGCTGCCCAATGCCCGAGGCTTCTCTCTGTGAAGAC	492
Db	141	ValMetValAspGlySerTrpGlyCysCysProMetProGlnAlaSerCysCysGluAsp	160
QY	493	AGSGTCACATGCTGTCCGACAGGTGCCTTCTGCGACCTGTGTCCACCCCGCTGCATCAC	552
Db	161	ArgValHisCysCysProHisGlyAlaPheCysAspLeuValHisThrArgCysIleThr	180
QY	553	CCGACGGGACCCACCCCTCGGCAAGAGCTCCCTGCCCGAGGACTACACGGGCA	612
Db	181	ProThrGlyThrHisProLeuAlaLysLysLeuProAlaGlnArgThrAsnArgAlaVal	200
QY	613	GCCTGTCCAGCTCGGTCATGTGTCGGGACGACGGTCCCGGTGCCCTGATGCTTCTACC	672
Db	201	AlaLeuSerSerSerValMetCysProAspAlaArgSerArgCysProAspGlySerThr	220
QY	673	TGCTGTGAGCTGCCAGTGGGAAGTATGGCTGTGTCGCCCAATGCCCAACGCCACCTGCTGC	732
Db	221	CysCysGluLeuProSerGlyLysTyrGlyCysCysProMetProAsnAlaThrCysCys	240
QY	733	TCCGATCACTGCATGCTGCCCGCCAGACACTGTGTGACCTGATPCAGAGTAAGTGC	792
Db	241	SerAspHisLeuHisCysCysProGlnAspThrValCysAspLeuIleGlySerLysCys	260

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; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996.488/P001-A
; CURRENT APPLICATION NUMBER: US/09/824, 807
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 08/991, 862
; PRIOR FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: 08/863, 862
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Human GP88 cDNA
US-09-824-807-17

Alignment Scores:
Pred. No.: 0 Length: 593
Score: 593.00 Matches: 593
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.45% Indels: 0
DB: 10 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-824-807-17 (1-593)
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QY 73 CCAGATGGTCAGTTCCTCCCTGTGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 132
DB 21 ProAspGlyGlnPheCysProValAlaCysCysLeuAspProGlyGlyAlaSerTyrSer 40
QY 133 TGCTGCGCTCCCTTCCTGGCAAAATGCCACACACTGACGAGCGCATCTGGTGGCGCCC 192
DB 41 CysCysArgProLeuLeuAspLysTrpProThrThrLeuSerArgHisLeuGlyGlyPro 60
QY 193 TGCCAGGTGTATGCCACTGTCTGTGCGGGCCACTCTGCACTCTGCACTCTGCACTCT 252
DB 61 CysGlnValAspAlaHisCysSerAlaGlyHisSerCysIlePheThrValSerGlyThr 80
QY 253 TCCAGTTGCTCCCTTCCAGAGCGCTGCGATGCGGGATGCGCATCTACTGTCGCCA 312
DB 81 SerSerCysCysProPheProGluAlaValAlaCysGlyAspGlyHisCysCysPro 100
QY 313 CGGGCTTCCACTGCAGTGCAGCGGGGATCTCTGCTTCCAAAGATCAGGTAACAATCC 372
DB 101 ArgGlyPheHisCysSerAlaAspGlyArgSerCysPheGlnArgSerGlyAsnSer 120
QY 373 GTGGGTGCCATCCAGTGCCTGTAGTCACTGCAATGCGCGGACTTCTCCACGTGTGT 432
DB 121 ValGlyAlaIleGlnCysProAspSerGlnPheGluCysProAspPheSerThrCysCys 140
QY 433 GTTATGTCGATGGCTCTGCGGGTGTGCTGCGCCATGCGCCAGGCTTCTGCTGTGAAG 492
DB 141 ValMetValAspGlySerTrpGlyCysCysProMetProGlnAlaSerCysCysGluasp 160
QY 493 AGGGTGCACCTGTGTCACGGTGCCTTCTGCGACCTGTTACACCCCGCTGCATCACA 552
DB 161 ArgValHisCysCysProHisGlyAlaPheCysAspLeuValHisThrArgCysIleThr 180
QY 553 CCCACGGGACCCACCCCTCGCAAGAGAGTCCCTGCCAGAGGACTTAACAGGCGCATG 612
DB 181 ProThrGlyThrHisProLeuAlaLysLysLeuProAlaGlnArgThrAsnArgAlaVal 200
QY 613 GCCTTGTCAGCTGGTCATGTGTCGCGACCGCGTCCCGTCCCTGTGCTGTGCTGTGCT 672
DB 201 AlaLeuSerSerValMetCysProAspAlaArgSerArgCysProAspGlySerThr 220
QY 673 TGCTGTGAGCTGCCAGTGGGAAGTATGGCTGCTGCCCAATGTCCTCCACCGCCACTGCTGC 732
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DB 221 CysCysGluLeuProSerGlyLysTyrGlyCysCysProMetProAsnAlaThrCysCys 240
QY 733 TCCGATCACCCTGCACTGCTGCCCCCAAGACACTGTGTGTACCTGATCCAGACTAGTGC 792
DB 241 SerAspHisLeuHisCysCysProGlnAspThrValCysAspLeuIleGlnSerLysCys 260
QY 793 CTCTCCAAGGAGAACGCTACACGGACCTCTCACTAAGCTGCTGCTGCGCACAGTGGGC 852
DB 261 LeuSerLysGluAsnAlaThrAspLeuLeuThrLysLeuProAlaHisThrValGly 280
QY 853 GATGTGAATGTGACATGGAGGTGAGCTGCCAGATGGCTATACCTGCTGCTGCTACAG 912
DB 281 AspValLysCysAspMetGluValSerCysProAspGlyTyrThrCysCysArgLeuGln 300
QY 913 TCCGGGGCTTGGGGCTGCTGCCCTTTTACCCAGCTGTGTGCTGAGGAGCACATACAC 972
DB 301 SerGlyAlaTrpGlyCysCysProPheThrGlnAlaValCysCysGluAspHisIleHis 320
QY 973 TGCTGTCCCGGGGTTTACGTGTGACACGACAGAGGGTACCTGTGTGAACAGGGCCCCAC 1032
DB 321 CysCysProAlaGlyPheThrCysAspThrGlnLysGlyThrCysGluGlnGlyProHis 340
QY 1033 CAGGTGCTGATGGAGAGGCCCGCCAGCTCACCTCAGCTGCGCAGACCCACAGCCCTG 1092
DB 341 GluValProTrpMetGluLysAlaProAlaHisLeuSerLeuProAspProGlnAlaLeu 360
QY 1093 AAGAGATGTCCCTGTGTATGTGTCAGAGCTGTCCCTCTCCGATACCTGCTGCGCAA 1152
DB 361 LysArgAspValProCysAspAsnValSerSerCysProSerAsnAspThrCysCysGln 380
QY 1153 CTCACGTCTGGGAGTGGGCTGCTGTCCAAATCCAGAGGCTGTCTGTCTGCTCGGACAC 1212
DB 381 LeuThrSerGlyGlnTrpGlyCysCysProIleProGluAlaValCysCysSerAspHis 400
QY 1213 CAGCACGTCTGCCCCCAGCGATACACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1272
DB 401 GlnHisCysCysProGlnArgTyrThrCysValAlaGluGlyGlnCysGlnArgGlySer 420
QY 1273 GAGATCTGGCTGCTGACAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1332
DB 421 GluIleValAlaGlyLeuGluLysMetProAlaArgArgGlySerLeuSerHisProArg 440
QY 1333 GACATCGCTGTGACACGACACAGCTGCCCGGTGGCGGAACTGTGTGTGTGTGTGTGT 1392
DB 441 AspIleGlyCysAspGlnHisThrSerCysProValGlyGlyThrCysCysProSerGln 460
QY 1393 GGTGGAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1452
DB 461 GlyGlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHis 480
QY 1453 TGCTGCGGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1512
DB 481 CysCysProAlaGlyTyrThrCysAsnValLysAlaArgSerProHisValGlyValLys 500
QY 1513 TCTGCCCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1572
DB 501 SerAlaGlnProAlaThrPheLeuAlaArgSerProHisValGlyValLysAspValGlu 520
QY 1573 TGTGGGGAGGACACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1632
DB 521 CysGlyGluGlyHisPheCysHisAspAsnGlnThrCysCysArgAspAsnArgGlnGly 540
QY 1633 TGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1692
DB 541 TrpAlaCysCysProTyrAlaGlnGlyValCysCysAlaAspArgArgHisCysCysPro 560
QY 1693 GCTGCTTCCCTGCGCAGCGGCTTACCAAGTGTGTTGCGCAGGAGGCGCGCGCTGCTG 1752
DB 561 AlaGlyPheArgCysAlaArgArgGlyThrLysCysLeuArgArgGluAlaProArgTrp 580
QY 1753 GACGCCCTTTTGGAGGACCCAGCCCTTGAGACAGCTGCTG 1791
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Db 581 AspAlaProLeuArgAspProAlaLeuArgGlnLeuLeu 593

RESULT 6

US-09-925-301-1416
; Sequence 1416, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05982
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1416
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1416

Alignment Scores:

Pred. No.:	0	Length:	621
Score:	410.00	Matches:	410
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	59.08%	Indels:	0
DB:	10	Gaps:	0

US-09-824-647-16 (1-2095) x US-09-925-301-1416 (1-621)

QY	1	CGCAGGACAGATGGTGGACCTGGTGGCTGCTTACAGCAGGCGCTGGTGGCT	60
Db	25	ArgArgGlnThrMetTrpThrLeuValSerTrpValAlaLeuThrAlaGlyLeuValAla	44
QY	61	GGAACGGGTGGCCAGATGGTCAAGTCTGCCCTGGCTGGCTGGCCGGAGGA	120
Db	45	GlyThrArgCysProAspGlyGlnPheCysProValAlaCysCysLeuAspProGlyGly	64
QY	121	GCCAGCTACAGCTGCTCCGCTCCCTTCTGGACAATGGCCCAACACATCAGCAGCAT	180
Db	65	AlaSerTrpSerCysCysArgProLeuLeuAspLysTrpProThrThrLeuSerArgHis	84
QY	181	CTGGTGGCCCTGCCAGGTGGATGCCACTGCTGCGGCCACTCTGTGATCTTACC	240
Db	85	LeuGlyGlyProCysGlnValAspAlaHisCysSerAlaGlyHisSerCysIlePheThr	104
QY	241	GTCTCAGGACTTCCAGTTGCTGCCCTTCCAGAGGCGGTGGCATGGGGGATGGCCAT	300
Db	105	ValSerGlyThrSerSerCysCysProPheProGluAlaValAlaCysGlyAspGlyHis	124
QY	301	CACCTGCTGCCAGCGGCTTCCACTGAGTGCACACGGCGCATCTCTTCCAAAGATCA	360
Db	125	HisCysCysProArgGlyPheHisCysSerAlaAspGlyArgSerCysPheGlnArgSer	144
QY	361	GGTAACAACTCCGGTGGCATCCAGTGCCTGATAGTTCGATGCGAATGCCCGGACTTC	420
Db	145	GlyAsnAsnSerValGlyAlaIleGlnCysProAspSerGlnPheGluCysProAspPhe	164
QY	421	TCCAGTGTGTTATGGTGGATGGCTCCGCGGGGTGGCTGCCCATGCCCGGCTTCC	480
Db	165	SerThrCysCysValMetValAspGlySerTrpGlyCysCysProMetProGlnAlaSer	184
QY	481	TGCTGTGAAGACGGTGCATGCTGTCGCGACGGTGCCTTCTCGGACCTGGTTCACACC	540
Db	185	CysCysGluAspArgValHisCysCysProHisGlyAlaPheCysAspLeuValHisThr	204
QY	541	CGCTGCATCACACCGGGGACCCACCCCTTGGCAAGAGCTCCCTGCCCGCAGGAGCT	600
Db	205	ArgCysIleThrProThrGlyThrHisProLeuAlaLysLysLeuProAlaGlnArgThr	224

QY	601	AACAGGCGAGTGGCTTGTCCAGCTCGCTCATGTCTCCGAGCGACGCTCCCGGTGCCCT	660
Db	225	AsnArgAlaValAlaLeuSerSerValMetCysProAspAlaArgSerArgCysPro	244
QY	661	GATGGTCTACCTGCTGTGAGCTGCCAGTGGGAAGTATGGCTGCTGCCAATGCCCAAC	720
Db	245	AspGlySerThrCysCysGluLeuProSerGlyLysTyrglyCysCysProMetProAn	264
QY	721	GCCACTGCTGCTCCGATCCTGACATGCTGCTGCCCAAGACACATGTGTGACCTGATC	780
Db	265	AlaThrCysCysSerAspHisLeuHisCysCysProGlnAspThrValCysAspLeuile	284
QY	781	CAGATTAAGTCCCTCTCCAAGGAGAACCTACCGAGGACCTCCTCCTCAAGCTGCTGG	840
Db	285	GlnSerLysCysLeuSerLysGluAsnAlaThrThrAspLeuLeuThrLysLeuProAla	304
QY	841	CACACAGTGGCGGATGTGAATGTACATGGAGGTGAGCTGCCAGATGGCTATACCTGC	900
Db	305	HisThrValGlyAspValLysCysAspMetGluValSerCysProAspGlyTrpThrCys	324
QY	901	TGCCGTCTACAGTCGGGGGCTGGGGCTGCTGCCCTTTTACCAGGCTGTGTGCTGTGAG	960
Db	325	CysArgLeuGlnSerGlyAlaTrpGlyCysCysProPheThrGlnAlaValCysCysGlu	344
QY	961	GACCACATACACTGCTGCTCCCGGGGTTAGTGTGACACGACAGGAGGTACCTGTGAA	1020
Db	345	AspHisIleHisCysCysProAlaGlyPheThrCysAspThrGlnLysGlyThrCysGlu	364
QY	1021	CAGGGGCCACACAGTGGCTGGAGTGGAGAGGCCAGCTCACCTCAGCTGCGCAGAC	1080
Db	365	GlnGlyProHisGlnValProTrpMetGluLysAlaProAlaHisLeuSerLeuProasp	384
QY	1081	CCACAAGCTTGAAGAGAGATGTCCCTGTGTATATGTACAGAGTGTCCCTCCTCCGAT	1140
Db	385	ProGlnAlaLeuLysArgAspValProCysAspAsnValSerSerCysProSerAsp	404
QY	1141	ACCTGCTCCCAACTCACCTGCTGGGAGTGGGCTGCTGCTCCCAATCCAGAGCTGCTGC	1200
Db	405	ThrCysCysGlnLeuThrSerGlyGluTrpGlyCysCysProIleProGluAlaValCys	424
QY	1201	TGCTCGGACACACAGCACTGCTGCCCGCCAG	1230
Db	425	CysSerAspHisGlnHisCysCysProGln	434

RESULT 7

US-09-864-761-43653
; Sequence 43653, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
; FILE REFERENCE: Aemica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 43653
LENGTH: 77
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC003043.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.65
OTHER INFORMATION: EST_HUMAN HIT: BF344549.1, EVALUE 8.00e-46
OTHER INFORMATION: SWISSPROT HIT: P28799, EVALUE 8.00e-47
US-09-864-761-43653

Alignment Scores:
Pred. No.: 8,26e-60 Length: 77
Score: 75.00 Matches: 75
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.81% Indels: 0
DB: 10 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-864-761-43653 (1-77)

QY 1426 GCTGTGCTGCGAGATGCCAGCAGCTGCTGCCGGTGGTACCTGCACTGAAG 1485
DB 1 AlaValCysCysGluAspArgGlnHisCysCysProAlaGlyTyrThrCysAsnVallys 20
QY 1486 GCTCATCTGCGAGAGAAAGTGTCTCTGCCAGCTGCCACCTTCTGCGCGTAGC 1545
DB 21 AlaArgSerCysGluLysGluValValSerAlaGlnProAlaThrPheLeuAlaArgSer 40
QY 1546 CTTCACTGGGTGTGAAGACCTGGAGTGTGGGAGGACACTTCTGCCATGATAACACG 1605
DB 41 ProHisValGlyVallysaspValGluCysGlyGluGlyHisPheCysHisaspGln 60
QY 1605 ACCTGCTGCCGACAGAACCGACAGGCTGGGCTGCTGCTCCCTAC 1650
DB 61 ThrCysCysArgAspAsnArgGlnGlyTyrPalaCysCysProTyr 75

RESULT 8

US-09-864-761-43654
Sequence 43654, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 43654
LENGTH: 48
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC003043.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.65
OTHER INFORMATION: EST_HUMAN HIT: BE742164.1, EVALUE 6.00e-20
US-09-864-761-43654

Alignment Scores:
Pred. No.: 3,5e-33 Length: 48
Score: 46.00 Matches: 46
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.69% Indels: 0
DB: 10 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-864-761-43654 (1-48)

QY 1650 GTAGGACAGCAGGCCAGCCCTGCTGCGCAGCAGGTCTGCTTATCATGGCA 1591
DB 3 ValGlyThrAlaGlyProAlaLeuSerValValSerAlaAlaGlyLeuValIleMeta 22
QY 1590 GAAGTGTCTTCCACACTCCACGCTTCTTACACCCAGCTACGGGCTACGGCCAGGAA 1531
DB 23 GluValSerPheProThrLeuHisValLeuHisThrHisValArgAlaThrGlyGlnGlu 42
QY 1530 GCTGGCAGGCTGGCAGA 1513
DB 43 GlyGlyArgLeuGlyArg 48
RESULT 9

US-09-874-056-4
; Sequence 4, Application US/09874056
; Publication No. US20020192704A1
; GENERAL INFORMATION:
; APPLICANT: OKANO, Akira
; APPLICANT: ETO, Yuzuru
; APPLICANT: IZUMI, Tetsuro
; TITLE OF INVENTION: Insulin Receptor-Related Receptor Binding Protein and Utilization
; FILE OF INVENTION: Same
; FILE REFERENCE: 209427050
; CURRENT APPLICATION NUMBER: US/09/874,056
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: JP 2000-170912
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-874-056-4

Alignment Scores:
Pred. No.: 2,37e-20 Length: 57
Score: 32.00 Matches: 32
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.61% Indels: 0
Gaps: 0
DB: 9

US-09-824-647-16 (1-2095) x US-09-874-056-4 (1-57)

QY 1396 GGGAGCTGGCGCTGCTGCCAGTGGCCCATGCTGTGTGCTGGAGGATGCCAGCACTGC 1455
; Sequence 5, Application US/09874056
; Publication No. US20020192704A1
; GENERAL INFORMATION:
; APPLICANT: OKANO, Akira
; APPLICANT: ETO, Yuzuru
; APPLICANT: IZUMI, Tetsuro
; TITLE OF INVENTION: Insulin Receptor-Related Receptor Binding Protein and Utilization
; FILE OF INVENTION: Same
; FILE REFERENCE: 209427050
; CURRENT APPLICATION NUMBER: US/09/874,056
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: JP 2000-170912
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-874-056-5

Alignment Scores:
Pred. No.: 2,36e-20 Length: 58
Score: 32.00 Matches: 32
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.61% Indels: 0
Gaps: 0
DB: 9

US-09-824-647-16 (1-2095) x US-09-874-056-5 (1-58)

QY 1396 GGGAGCTGGCGCTGCTGCCAGTGGCCCATGCTGTGTGCTGGAGGATGCCAGCACTGC 1455
; Sequence 5, Application US/09874056
; Publication No. US20020192704A1
; GENERAL INFORMATION:
; APPLICANT: OKANO, Akira
; APPLICANT: ETO, Yuzuru
; APPLICANT: IZUMI, Tetsuro
; TITLE OF INVENTION: Insulin Receptor-Related Receptor Binding Protein and Utilization
; FILE OF INVENTION: Same
; FILE REFERENCE: 209427050
; CURRENT APPLICATION NUMBER: US/09/874,056
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: JP 2000-170912
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-874-056-5

Alignment Scores:
Pred. No.: 2,36e-20 Length: 58
Score: 32.00 Matches: 32
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.61% Indels: 0
Gaps: 0
DB: 9

US-09-824-647-16 (1-2095) x US-09-874-056-5 (1-58)

QY 1396 GGGAGCTGGCGCTGCTGCCAGTGGCCCATGCTGTGTGCTGGAGGATGCCAGCACTGC 1455
; Sequence 5, Application US/09874056
; Publication No. US20020192704A1
; GENERAL INFORMATION:
; APPLICANT: OKANO, Akira
; APPLICANT: ETO, Yuzuru
; APPLICANT: IZUMI, Tetsuro
; TITLE OF INVENTION: Insulin Receptor-Related Receptor Binding Protein and Utilization
; FILE OF INVENTION: Same
; FILE REFERENCE: 209427050
; CURRENT APPLICATION NUMBER: US/09/874,056
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: JP 2000-170912
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-874-056-7

US-09-824-647-16 (1-2095) x US-09-874-056-7 (1-58)

QY 1396 GGGAGCTGGCGCTGCTGCCAGTGGCCCATGCTGTGTGCTGGAGGATGCCAGCACTGC 1455
; Sequence 5, Application US/09874056
; Publication No. US20020192704A1
; GENERAL INFORMATION:
; APPLICANT: OKANO, Akira
; APPLICANT: ETO, Yuzuru
; APPLICANT: IZUMI, Tetsuro
; TITLE OF INVENTION: Insulin Receptor-Related Receptor Binding Protein and Utilization
; FILE OF INVENTION: Same
; FILE REFERENCE: 209427050
; CURRENT APPLICATION NUMBER: US/09/874,056
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: JP 2000-170912
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-874-056-7

Alignment Scores:
Pred. No.: 2,36e-20 Length: 58
Score: 32.00 Matches: 32
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.61% Indels: 0
Gaps: 0
DB: 9

US-09-824-647-16 (1-2095) x US-09-874-056-7 (1-58)

QY 1396 GGGAGCTGGCGCTGCTGCCAGTGGCCCATGCTGTGTGCTGGAGGATGCCAGCACTGC 1455
; Sequence 5, Application US/09874056
; Publication No. US20020192704A1
; GENERAL INFORMATION:
; APPLICANT: OKANO, Akira
; APPLICANT: ETO, Yuzuru
; APPLICANT: IZUMI, Tetsuro
; TITLE OF INVENTION: Insulin Receptor-Related Receptor Binding Protein and Utilization
; FILE OF INVENTION: Same
; FILE REFERENCE: 209427050
; CURRENT APPLICATION NUMBER: US/09/874,056
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: JP 2000-170912
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-874-056-7

US-09-824-647-16 (1-2095) x US-09-874-056-7 (1-58)

QY 1396 GGGAGCTGGCGCTGCTGCCAGTGGCCCATGCTGTGTGCTGGAGGATGCCAGCACTGC 1455
; Sequence 5, Application US/09874056
; Publication No. US20020192704A1
; GENERAL INFORMATION:
; APPLICANT: OKANO, Akira
; APPLICANT: ETO, Yuzuru
; APPLICANT: IZUMI, Tetsuro
; TITLE OF INVENTION: Insulin Receptor-Related Receptor Binding Protein and Utilization
; FILE OF INVENTION: Same
; FILE REFERENCE: 209427050
; CURRENT APPLICATION NUMBER: US/09/874,056
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: JP 2000-170912
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-874-056-7

Alignment Scores:
Pred. No.: 1,73e-20 Length: 589

Score: 32.00 Matches: 32
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.61% Indels: 0
DB: Gaps: 0

US-09-824-647-16 (1-2095) x US-09-824-647-2 (1-589)

QY 1396 GGGAGCTGGCGCTGCTGCCAGTGGCCCATGCTGTGTGCTGGCAGGATGCCGAGCACTGC 1455
|||||
Db 460 GlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHisCys 479
QY 1456 TGCCCGGCTGGCTACACCTGCAAGCTGAAGGCTCGA 1491
|||||
Db 480 CysProAlaGlyTyrThrCysAsnValLysAlaArg 491

RESULT 13

US-10-218-509-2
; Sequence 2, Application US/10218509
; Publication No. US20030092661A1
; GENERAL INFORMATION:
; APPLICANT: Sertero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996.488/P001-A
; CURRENT APPLICATION NUMBER: US/10/218,509
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 08/991,862
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 589
; TYPE: PRT
; ORGANISM: Mouse epithelin/granulin
US-10-218-509-2

Alignment Scores:
Pred. No.: 1.73e-20 Length: 589
Score: 32.00 Matches: 32
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.61% Indels: 0
DB: Gaps: 0

US-09-824-647-16 (1-2095) x US-10-218-509-2 (1-589)

QY 1396 GGGAGCTGGCGCTGCTGCCAGTGGCCCATGCTGTGTGCTGGCAGGATGCCGAGCACTGC 1455
|||||
Db 460 GlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHisCys 479
QY 1456 TGCCCGGCTGGCTACACCTGCAAGCTGAAGGCTCGA 1491
|||||
Db 480 CysProAlaGlyTyrThrCysAsnValLysAlaArg 491

RESULT 14

US-10-281-160-2
; Sequence 2, Application US/10281160
; Publication No. US20030108950A1
; GENERAL INFORMATION:
; APPLICANT: Sertero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996.488/P001-A
; CURRENT APPLICATION NUMBER: US/10/281,160
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/08/991,862
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2

; LENGTH: 589
; TYPE: PRT
; ORGANISM: Mouse epithelin/granulin
US-10-281-160-2

Alignment Scores:
Pred. No.: 1.73e-20 Length: 589
Score: 32.00 Matches: 32
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.61% Indels: 0
DB: Gaps: 0

US-09-824-647-16 (1-2095) x US-10-281-160-2 (1-589)

QY 1396 GGGAGCTGGCGCTGCTGCCAGTGGCCCATGCTGTGTGCTGGCAGGATGCCGAGCACTGC 1455
|||||
Db 460 GlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHisCys 479
QY 1456 TGCCCGGCTGGCTACACCTGCAAGCTGAAGGCTCGA 1491
|||||
Db 480 CysProAlaGlyTyrThrCysAsnValLysAlaArg 491

RESULT 15

US-09-813-156-2
; Sequence 2, Application US/09813156
; Patent No. US20020061859A1
; GENERAL INFORMATION:
; APPLICANT: Sertero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996.488/P001-A
; CURRENT APPLICATION NUMBER: US/09/813,156
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 08/991,862
; PRIOR FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 589
; TYPE: PRT
; ORGANISM: Mouse epithelin/granulin
US-09-813-156-2

Alignment Scores:
Pred. No.: 1.73e-20 Length: 589
Score: 32.00 Matches: 32
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.61% Indels: 0
DB: Gaps: 0

US-09-824-647-16 (1-2095) x US-09-813-156-2 (1-589)

QY 1396 GGGAGCTGGCGCTGCTGCCAGTGGCCCATGCTGTGTGCTGGCAGGATGCCGAGCACTGC 1455
|||||
Db 460 GlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHisCys 479
QY 1456 TGCCCGGCTGGCTACACCTGCAAGCTGAAGGCTCGA 1491
|||||
Db 480 CysProAlaGlyTyrThrCysAsnValLysAlaArg 491

RESULT 16

US-09-824-807-2
; Sequence 2, Application US/09824807
; Patent No. US20020094966A1
; GENERAL INFORMATION:
; APPLICANT: Sertero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996.488/P001-A
; CURRENT APPLICATION NUMBER: US/09/824,807
; CURRENT FILING DATE: 2001-04-04

;; PRIOR APPLICATION NUMBER: 08/991,862
;; PRIOR FILING DATE: 1997-12-16
;; PRIOR APPLICATION NUMBER: 08/863,862
;; PRIOR FILING DATE: 1997-05-23
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 2
;; LENGTH: 589
;; TYPE: PRT
;; ORGANISM: Mouse epithelin/granulin
US-09-824-807-2

Alignment Scores:
Pred. No.: 1-73e-20 Length: 589
Score: 32.00 Matches: 32
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.61% Indels: 0
DB: 10 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-824-807-2 (1-589)

QY 1396 GGGAGCTGGCCGCTGCCAGTTCGCCAGTCTGTGTCGCGAGGATGCCAGCACTGC 1455
|||||
Db 460 GlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGlnAspArgGlnHisCys 479
QY 1456 TGGCGGCTGGTACACCTCCACGTCACGTCGAGGCTCGA 1491
|||||
Db 480 CysProAlaGlyTrpThrCysAsnValLysAlaArg 491

RESULT 17

US-09-824-647-6
;; Sequence 6, Application US/09824647
;; Publication No. US20020183270A1
;; GENERAL INFORMATION:
;; APPLICANT: Serrero, Ginette
;; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
;; FILE REFERENCE: 29996.488/P001-A
;; CURRENT APPLICATION NUMBER: US/09/824,647
;; PRIOR FILING DATE: 2001-04-04
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,862
;; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/863,862
;; PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 6
;; LENGTH: 19
;; TYPE: PRT
;; ORGANISM: Human granulin
;; FEATURE:
;; NAME/KEY: PEPTIDE
;; LOCATION: (1)..(19)
;; OTHER INFORMATION: Internal peptide of human GP88 used to develop
;; OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody.
US-09-824-647-6

Alignment Scores:
Pred. No.: 2.3e-08 Length: 19
Score: 19.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.74% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-824-647-6 (1-19)

QY 1048 GAGAGCCCGCCAGCTCAGCTGCCAGCCACCAAGCCTTGAAGAGAGATGTC 1104
|||||
Db 1 GlulysAlaProAlaHisLeuSerLeuProAspProGlnAlaLeuLysArgAspVal 19
RESULT 18
US-10-218-509-6

;; Sequence 6, Application US/10218509
;; Publication No. US20030092661A1
;; GENERAL INFORMATION:
;; APPLICANT: Serrero, Ginette
;; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
;; FILE REFERENCE: 29996.488/P001-A
;; CURRENT APPLICATION NUMBER: US/10/218,509
;; CURRENT FILING DATE: 2002-08-15
;; PRIOR APPLICATION NUMBER: 08/991,862
;; PRIOR FILING DATE: 1998-08-17
;; PRIOR APPLICATION NUMBER: 08/863,862
;; PRIOR FILING DATE: 1997-05-23
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 6
;; LENGTH: 19
;; TYPE: PRT
;; ORGANISM: Human granulin
;; FEATURE:
;; NAME/KEY: PEPTIDE
;; LOCATION: (1)..(19)
;; OTHER INFORMATION: Internal peptide of human GP88 used to develop
;; OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody.
US-10-218-509-6

Alignment Scores:
Pred. No.: 2.3e-08 Length: 19
Score: 19.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.74% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-10-218-509-6 (1-19)

QY 1048 GAGAGCCCGCCAGCTCAGCTGCCAGCCACCAAGCCTTGAAGAGAGATGTC 1104
|||||
Db 1 GlulysAlaProAlaHisLeuSerLeuProAspProGlnAlaLeuLysArgAspVal 19

RESULT 19

US-10-281-160-6
;; Sequence 6, Application US/10281160
;; Publication No. US20030108950A1
;; GENERAL INFORMATION:
;; APPLICANT: Serrero, Ginette
;; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
;; FILE REFERENCE: 29996.488/P001-A
;; CURRENT APPLICATION NUMBER: US/10/281,160
;; CURRENT FILING DATE: 2002-10-28
;; PRIOR APPLICATION NUMBER: 08/991,862
;; PRIOR FILING DATE: 1998-08-17
;; PRIOR APPLICATION NUMBER: 08/863,862
;; PRIOR FILING DATE: 1997-05-23
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 6
;; LENGTH: 19
;; TYPE: PRT
;; ORGANISM: Human granulin
;; FEATURE:
;; NAME/KEY: PEPTIDE
;; LOCATION: (1)..(19)
;; OTHER INFORMATION: Internal peptide of human GP88 used to develop
;; OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody.
US-10-281-160-6

Alignment Scores:
Pred. No.: 2.3e-08 Length: 19
Score: 19.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.74% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-10-281-160-6 (1-19)

QY 1048 GAGAAGCCCCAGCTCAGCTCCAGTCCAGACCCACAGCCTTGAGAGAGATGTC 1104
Db 1 GlulysAlaProAlaHisLeuSerLeuProAspProGlnAlaLeuLysArgAspVal 19

RESULT 20

US-09-813-156-6
; Sequence 6, Application US/09813156
; Patent No. US20020061859A1
; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: Z9996.488/P001-A
; CURRENT APPLICATION NUMBER: US/09/813,156
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 08/991,862
; PRIOR FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Human granulin
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(19)
; OTHER INFORMATION: Internal peptide of human GP88 used to develop
; neutralizing anti-human GP88 monoclonal antibody.
US-09-813-156-6

Alignment Scores:
Pred. No.: 2 3e-08 Length: 19
Score: 19.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.74% Indels: 0
DB: 10 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-813-156-6 (1-19)

QY 1048 GAGAAGCCCCAGCTCAGCTCCAGTCCAGACCCACAGCCTTGAGAGAGATGTC 1104
Db 1 GlulysAlaProAlaHisLeuSerLeuProAspProGlnAlaLeuLysArgAspVal 19

RESULT 21

US-09-824-807-6
; Sequence 6, Application US/09824807
; Patent No. US20020094966A1
; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: Z9996.488/P001-A
; CURRENT APPLICATION NUMBER: US/09/824,807
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 08/991,862
; PRIOR FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Human granulin
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(19)
; OTHER INFORMATION: Internal peptide of human GP88 used to develop
; neutralizing anti-human GP88 monoclonal antibody.

US-09-824-807-6

Alignment Scores:
Pred. No.: 2 3e-08 Length: 19
Score: 19.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.74% Indels: 0
DB: 10 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-824-807-6 (1-19)

QY 1048 GAGAAGCCCCAGCTCAGCTCCAGTCCAGACCCACAGCCTTGAGAGAGATGTC 1104
Db 1 GlulysAlaProAlaHisLeuSerLeuProAspProGlnAlaLeuLysArgAspVal 19

RESULT 22

US-09-874-056-3
; Sequence 3, Application US/09874056
; Publication No. US20020192704A1
; GENERAL INFORMATION:
; APPLICANT: OKANO, Akira
; APPLICANT: ETO, Yuzuru
; APPLICANT: IZUMI, Tetsuro
; TITLE OF INVENTION: Insulin Receptor-Related Receptor Binding Protein and Utilizat
; TITLE OF INVENTION: Same
; FILE REFERENCE: 209427USO
; CURRENT APPLICATION NUMBER: US/09/874,056
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: JP 2000-170912
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-874-056-3

Alignment Scores:
Pred. No.: 1 36e-06 Length: 57
Score: 17.00 Matches: 17
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.45% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-874-056-3 (1-57)

QY 1396 GGGAGCTGGCTGCTGCCAGTGGCCAGTGGCCCATGCTGTGTGTCGAGGATGCG 1446
Db 22 GlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArg 38

RESULT 23

US-09-874-056-6
; Sequence 6, Application US/09874056
; Publication No. US20020192704A1
; GENERAL INFORMATION:
; APPLICANT: OKANO, Akira
; APPLICANT: ETO, Yuzuru
; APPLICANT: IZUMI, Tetsuro
; TITLE OF INVENTION: Insulin Receptor-Related Receptor Binding Protein and Utiliza
; TITLE OF INVENTION: Same
; FILE REFERENCE: 209427USO
; CURRENT APPLICATION NUMBER: US/09/874,056
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: JP 2000-170912
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 59
; TYPE: PRT

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; ORGANISM: Mus musculus
US-09-874-056-6

Alignment Scores:
Pred. No.: 1.12e-05 Length: 59
Score: 16.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.31% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-874-056-6 (1-59)
QY 1396 GCGAGTGGCCGTCGACAGTGTCCGAGGAGCCCGCGGC 1443
Db 22 GlysertrpAlaCysGlnLeuProHisAlaValCysCysGluasp 37

RESULT 24
US-09-824-647-7
; Sequence 7, Application US/09824647
; Publication No. US20020183270A1
; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996.488/P001-A
; CURRENT APPLICATION NUMBER: US/09/824,647
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,862
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Human granulin
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(14)
; OTHER INFORMATION: Internal peptide of human GP88 used to develop
; neutralizing anti-human GP88 monoclonal antibody.
US-09-824-647-7

Alignment Scores:
Pred. No.: 0.000925 Length: 14
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-824-647-7 (1-14)
QY 1708 GCAGCAGGGGTACCAAGTGTTCGCGAGGAGCCCGCGGC 1749
Db 1 AlaAargGlyThrLysCysLeuAargGluAlaProarg 14

RESULT 25
US-10-218-509-7
; Sequence 7, Application US/10218509
; Publication No. US20030092661A1
; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996.488/P001-A
; CURRENT APPLICATION NUMBER: US/10/218,509
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 08/991,862
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Human granulin
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(14)
; OTHER INFORMATION: Internal peptide of human GP88 used to develop
; neutralizing anti-human GP88 monoclonal antibody.
US-09-824-647-7

Alignment Scores:
Pred. No.: 0.000925 Length: 14
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-10-218-509-7 (1-14)
QY 1708 GCAGCAGGGGTACCAAGTGTTCGCGAGGAGCCCGCGGC 1749
Db 1 AlaAargGlyThrLysCysLeuAargGluAlaProarg 14

RESULT 26
US-10-281-160-7
; Sequence 7, Application US/10281160
; Publication No. US20030108950A1
; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996.488/P001-A
; CURRENT APPLICATION NUMBER: US/10/281,160
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/08/991,862
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Human granulin
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(14)
; OTHER INFORMATION: Internal peptide of human GP88 used to develop
; neutralizing anti-human GP88 monoclonal antibody.
US-10-281-160-7

Alignment Scores:
Pred. No.: 0.000925 Length: 14
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-10-281-160-7 (1-14)
QY 1708 GCAGCAGGGGTACCAAGTGTTCGCGAGGAGCCCGCGGC 1749
Db 1 AlaAargGlyThrLysCysLeuAargGluAlaProarg 14

RESULT 27
US-09-813-156-7
; Sequence 7, Application US/09813156
; Patent No. US20020061859A1
; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
```

;; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
;; FILE REFERENCE: 29996.488/P001-A
;; CURRENT APPLICATION NUMBER: US/09/813.156
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 08/991.862
;; PRIOR FILING DATE: 1997-12-16
;; PRIOR APPLICATION NUMBER: 08/863.862
;; PRIOR FILING DATE: 1997-05-23
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 7
;; LENGTH: 14
;; TYPE: PRT
;; ORGANISM: Human granulin
;; FEATURE:
;; NAME/KEY: PEPTIDE
;; LOCATION: (1)..(14)
;; OTHER INFORMATION: Internal peptide of human GP88 used to develop
;; OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody.
US-09-813-156-7

Alignment Scores:
Pred. No.: 0.000925 Length: 14
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 10 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-813-156-7 (1-14)
QY 1708 GCAGCAGGGGTACCAAGTGTTCGCCAGGAGGCCCGCGC 1749
Db 1 AlaArgArgGlyThrLysCysLeuArgArgGluAlaProArg 14

RESULT 28
US-09-824-807-7
;; Sequence 7, Application US/09824807
;; Patent No. US20020094966A1
;; GENERAL INFORMATION:
;; APPLICANT: Seriero, Ginette
;; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
;; FILE REFERENCE: 29996.488/P001-A
;; CURRENT APPLICATION NUMBER: US/09/824.807
;; CURRENT FILING DATE: 2001-04-04
;; PRIOR APPLICATION NUMBER: 08/991.862
;; PRIOR FILING DATE: 1997-12-16
;; PRIOR APPLICATION NUMBER: 08/863.862
;; PRIOR FILING DATE: 1997-05-23
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 7
;; LENGTH: 14
;; TYPE: PRT
;; ORGANISM: Human granulin
;; FEATURE:
;; NAME/KEY: PEPTIDE
;; LOCATION: (1)..(14)
;; OTHER INFORMATION: Internal peptide of human GP88 used to develop
;; OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody.
US-09-824-807-7

Alignment Scores:
Pred. No.: 0.000925 Length: 14
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 10 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-824-807-7 (1-14)
QY 1708 GCAGCAGGGGTACCAAGTGTTCGCCAGGAGGCCCGCGC 1749

Db 1 AlaArgArgGlyThrLysCysLeuArgArgGluAlaProArg 14
RESULT 29
US-09-809-545A-43
;; Sequence 43, Application US/09809545A
;; Patent No. US20020110804A1
;; GENERAL INFORMATION:
;; APPLICANT: Stanton, Lawrence W.
;; APPLICANT: White, R. Tyler
;; TITLE OF INVENTION: SECRETED FACTORS
;; FILE REFERENCE: SCIOS.017A
;; CURRENT APPLICATION NUMBER: US/09/809.545A
;; CURRENT FILING DATE: 2001-03-14
;; NUMBER OF SEQ ID NOS: 84
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 43
;; LENGTH: 46
;; TYPE: PRT
;; ORGANISM: Rattus norvegicus
US-09-809-545A-43

Alignment Scores:
Pred. No.: 251 Length: 46
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 10 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-809-545A-43 (1-46)
QY 494 CTGCTTTCACAGCAGGAGCCTGG 471
Db 25 LeuSerSerGlnGlnGluAlaTrp 32

RESULT 30
US-09-764-877-1593
;; Sequence 1593, Application US/09764877
;; Patent No. US20020147140A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PC005
;; CURRENT APPLICATION NUMBER: US/09/764.877
;; CURRENT FILING DATE: 2001-01-17
;; PRIOR application data removed - refer to PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 4031
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1593
;; LENGTH: 60
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (19)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-877-1593

Alignment Scores:
Pred. No.: 242 Length: 60
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 10 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-764-877-1593 (1-60)
QY 1022 AGGGGCCCCACAGGTCCTCGGA 1045
Db 3 ArgGlyProThrArgCysProGly 10

RESULT 31
US-10-039-836A-2
; Sequence 2, Application US/10039836A
; Publication No. US20030033632A1
; GENERAL INFORMATION:
; APPLICANT: Crane, Virginia
; APPLICANT: Simmons, Carl
; TITLE OF INVENTION: Maize Proteinase Inhibitor-Like
; FILE REFERENCE: 35718/239836
; CURRENT APPLICATION NUMBER: US/10/039,836A
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/243,167
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Zea mays
US-10-039-836A-2

Alignment Scores:
Pred. No.: 227 Length: 97
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-10-039-836A-2 (1-97)
QY 1455 GCAGTCTGGCGATCTCGCAGCA 1432
Db 12 AlavalLeuAlaIleLeuAlaIle 19

RESULT 32
US-09-925-301-1558
; Sequence 1558, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1558
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (80)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (101)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (107)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (108)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1558

Alignment Scores:
Pred. No.: 223 Length: 109

Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 10 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-925-301-1558 (1-109)
QY 1006 AGGGTACCTGTGAACAGGGGCC 1029
Db 57 LysGlyThrCysGluGlnGlyPro 64

RESULT 33
US-09-934-465-11
; Sequence 11, Application US/09934465
; Patent No. US20020102233A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/09/934,465
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 08/584,031
; PRIOR FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-465-11

Alignment Scores:
Pred. No.: 214 Length: 151
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 10 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-934-465-11 (1-151)
QY 1734 CAGGAGGCCCGCGCTGGGACGC 1757
Db 32 GlnGlyGlyProAlaLeuGlyArg 39

RESULT 34
US-10-237-271-18
; Sequence 18, Application US/10237271
; Publication No. US20030096328A1
; GENERAL INFORMATION:
; APPLICANT: THE BURNHAM INSTITUTE
; APPLICANT: SMITH, Jeffrey W.
; APPLICANT: KRIDEL, Steven J.
; APPLICANT: AXELROD, Fumiko T.
; TITLE OF INVENTION: SERINE/THREONINE HYDROLASE PROTEINS AND SCREENING ASSAYS
; FILE REFERENCE: BURN1100-1
; CURRENT APPLICATION NUMBER: US/10/237,271
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 60/317,842
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (3)...(8)
; OTHER INFORMATION: Xaa is any Amino Acid
; FEATURE:
; NAME/KEY: MISC_FEATURE

us-09-824-647-16.std.rapb

Tue Jul 8 07:45:14 2003

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; LOCATION: (32)..(56)
; OTHER INFORMATION: xaa is any Amino Acid
US-10-237-271-18

Alignment Scores:
Pred. No.: 211 Length: 166
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-10-237-271-18 (1-166)

QY 1686 CTGCTCGTGGCTCCGTCGGCGC 1709
Db 78 LeuSerCysTrpLeuProLeuArg 85

RESULT 35
US-10-156-761-12579
; Sequence 12579, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASHIARA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10156761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 12579
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12579

Alignment Scores:
Pred. No.: 207 Length: 190
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-10-156-761-12579 (1-190)

QY 936 AGGCAGCAGCCCGCCAGCCCGCA 913
Db 49 ArgAlaAlaAlaProGlyProArg 56

RESULT 36
US-10-245-103-48
; Sequence 48, Application US/10245103
; Publication No. US20030068778A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Collin
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P363081C71
; CURRENT APPLICATION NUMBER: US/10/245,107
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942

; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P363081C112
; CURRENT APPLICATION NUMBER: US/10/245,103
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 48
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-103-48

Alignment Scores:
Pred. No.: 207 Length: 192
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-10-245-103-48 (1-192)

QY 794 TCTCAGGAGAGCTACCACGG 817
Db 2 SerProArgThrLeuProArg 9

RESULT 37
US-10-245-107-48
; Sequence 48, Application US/10245107
; Publication No. US20030068779A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Collin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P363081C71
; CURRENT APPLICATION NUMBER: US/10/245,107
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942

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;; PRIOR FILING DATE: 2002-07-18
;; PRIOR APPLICATION NUMBER: 60/059114
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/063046
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/065027
;; PRIOR FILING DATE: 1997-11-10
;; PRIOR APPLICATION NUMBER: 60/079689
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/086478
;; PRIOR FILING DATE: 1998-05-22
;; PRIOR APPLICATION NUMBER: 60/087607
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/089801
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090689
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 116
;; SEQ ID NO 48
;; LENGTH: 192
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-245-107-48

Alignment Scores:
Pred. No.: 207 Length: 192
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-10-245-107-48 (1-192)

QY 794 TCTCAAGGAGAACCTACCACGG 817
Db 2 SerProArgThrLeuProArg 9
|||||

RESULT 38

US-10-245-143-48
;; Sequence 48, Application US/10245143
;; Publication No. US20030068780A1
;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin
;; APPLICANT: Eaton, Dan
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin
;; APPLICANT: Smith, Victoria
;; APPLICANT: Stephan, Jean-Phillippe
;; APPLICANT: Watanabe, Colin
;; APPLICANT: Wood, William
;; APPLICANT: Zhang, Zemin
;; APPLICANT: Fong, Sherman
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P363081C90
;; CURRENT APPLICATION NUMBER: US/10/245,143
;; CURRENT FILING DATE: 2002-09-16
;; PRIOR APPLICATION NUMBER: 10/197942
;; PRIOR FILING DATE: 2002-07-18
;; PRIOR APPLICATION NUMBER: 60/059114
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/063046
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/065027
;; PRIOR FILING DATE: 1997-11-10
;; PRIOR APPLICATION NUMBER: 60/079689
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/086478
;; PRIOR FILING DATE: 1998-05-22
;; PRIOR APPLICATION NUMBER: 60/087607
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/089801
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090689

;; PRIOR APPLICATION NUMBER: 60/086478
;; PRIOR FILING DATE: 1998-05-22
;; PRIOR APPLICATION NUMBER: 60/087607
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/089801
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090689
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 116
;; SEQ ID NO 48
;; LENGTH: 192
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-245-143-48

Alignment Scores:
Pred. No.: 207 Length: 192
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-10-245-143-48 (1-192)

QY 794 TCTCAAGGAGAACCTACCACGG 817
Db 2 SerProArgThrLeuProArg 9
|||||

RESULT 39

US-10-245-771-48
;; Sequence 48, Application US/10245771
;; Publication No. US20030068781A1
;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin
;; APPLICANT: Eaton, Dan
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin
;; APPLICANT: Smith, Victoria
;; APPLICANT: Stephan, Jean-Phillippe
;; APPLICANT: Watanabe, Colin
;; APPLICANT: Wood, William
;; APPLICANT: Zhang, Zemin
;; APPLICANT: Fong, Sherman
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P363081C98
;; CURRENT APPLICATION NUMBER: US/10/245,771
;; CURRENT FILING DATE: 2002-09-16
;; PRIOR APPLICATION NUMBER: 10/197942
;; PRIOR FILING DATE: 2002-07-18
;; PRIOR APPLICATION NUMBER: 60/059114
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/063046
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/065027
;; PRIOR FILING DATE: 1997-11-10
;; PRIOR APPLICATION NUMBER: 60/079689
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/086478
;; PRIOR FILING DATE: 1998-05-22
;; PRIOR APPLICATION NUMBER: 60/087607
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/089801
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090689

us-09-824-647-16.std.rapb

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Alignment Scores: 207 Length: 192

Pred. No.: 8.00 Matches: 8

Score: 100.00% Conservatives: 0

Percent Similarity: 100.00% Mismatches: 0

Best Local Similarity: 100.00% Indels: 0

Query Match: 1.15% Gaps: 0

DB: 9

US-09-824-647-16 (1-2095) x US-10-245-771-48 (1-192)

QY 794 TCTCCAGGAGACGCTACCGG 817

Db 2 SerProArgThrLeuProArg 9

RESULT 40

US-10-245-851-48

Sequence 48, Application US/10245851

Publication No. US20030068782A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Eaton, Dan

APPLICANT: Filvaroff, Ellen

APPLICANT: Goddard, Audrey

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Phillippe

APPLICANT: Watanabe, Colin

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

APPLICANT: Fong, Sherman

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3630R1C70

CURRENT APPLICATION NUMBER: US/10/245,851

CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: 10/197942

PRIOR FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/059114

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/063046

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/065027

PRIOR FILING DATE: 1997-11-10

PRIOR APPLICATION NUMBER: 60/079689

PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/086478

PRIOR FILING DATE: 1998-05-22

PRIOR APPLICATION NUMBER: 60/087607

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/089801

PRIOR FILING DATE: 1998-06-18

PRIOR APPLICATION NUMBER: 60/090557

PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090689

PRIOR FILING DATE: 1998-06-25

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 116

SEQ ID NO 48

LENGTH: 192

TYPE: PRT

ORGANISM: Homo Sapien

US-10-245-851-48

Alignment Scores: 207 Length: 192

Pred. No.: 8.00 Matches: 8

Score: 100.00% Conservatives: 0

Percent Similarity: 100.00% Mismatches: 0

Best Local Similarity: 100.00% Indels: 0

Query Match: 1.15% Gaps: 0

DB: 9

US-09-824-647-16 (1-2095) x US-10-245-851-48 (1-192)

QY 794 TCTCCAGGAGACGCTACCGG 817

Db 2 SerProArgThrLeuProArg 9

RESULT 41

US-10-245-883-48

Sequence 48, Application US/10245883

Publication No. US20030068783A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Eaton, Dan

APPLICANT: Filvaroff, Ellen

APPLICANT: Goddard, Audrey

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Phillippe

APPLICANT: Watanabe, Colin

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

APPLICANT: Fong, Sherman

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3630R1C70

CURRENT APPLICATION NUMBER: US/10/245,883

CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: 10/197942

PRIOR FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/059114

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/063046

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/065027

PRIOR FILING DATE: 1997-11-10

PRIOR APPLICATION NUMBER: 60/079689

PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/086478

PRIOR FILING DATE: 1998-05-22

PRIOR APPLICATION NUMBER: 60/087607

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/089801

PRIOR FILING DATE: 1998-06-18

PRIOR APPLICATION NUMBER: 60/090557

PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090689

PRIOR FILING DATE: 1998-06-25

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 116

SEQ ID NO 48

LENGTH: 192

TYPE: PRT

ORGANISM: Homo Sapien

US-10-245-883-48

Alignment Scores: 207 Length: 192

Pred. No.: 8.00 Matches: 8

Score: 100.00% Conservatives: 0

Percent Similarity: 100.00% Mismatches: 0

Best Local Similarity: 100.00% Indels: 0

Query Match: 1.15% Gaps: 0

DB: 9

US-09-824-647-16 (1-2095) x US-10-245-883-48 (1-192)

OY 794 TCTCAAGGAGGACGCTACCACGG 817
Db 2 SerProargargthrluProarg 9
RESULT 42
US-10-237-535-48
Sequence 48, Application US/10237535
Publication No. US20030073188A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C3
CURRENT APPLICATION NUMBER: US/10/237,535
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091358
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/106932
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/115554
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119342
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/123957
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123972
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: 60/127372
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/131271
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/133459
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/135725
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/135729
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/135750
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/138385
PRIOR FILING DATE: 1999-06-09
PRIOR APPLICATION NUMBER: 60/140653
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144732
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/144790
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145228
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146843
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/148188
PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/148513
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/149327
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149395
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/150114
PRIOR FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: 60/151700
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/151734
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/162506
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 60/170262
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 60/177118
PRIOR FILING DATE: 2000-01-20
PRIOR APPLICATION NUMBER: 60/179851
PRIOR FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: 60/180921
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: 60/187202
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/198587
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 60/199614
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 60/206330
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206368
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/209832
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 60/218371
PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 60/222695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/229896
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/230621
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/232887
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/235147
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/261878
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/261910

PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: 60/261939
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: 60/262150
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: 60/264395
 PRIOR FILING DATE: 2001-01-25
 PRIOR APPLICATION NUMBER: 60/266421
 PRIOR FILING DATE: 2001-02-02
 PRIOR APPLICATION NUMBER: 60/267623
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/274399
 PRIOR FILING DATE: 2001-03-09
 PRIOR APPLICATION NUMBER: 60/280982
 PRIOR FILING DATE: 2001-04-03
 PRIOR APPLICATION NUMBER: 60/282129
 PRIOR FILING DATE: 2001-04-04
 PRIOR APPLICATION NUMBER: 60/282199
 PRIOR FILING DATE: 2001-04-04
 PRIOR APPLICATION NUMBER: 60/290589
 PRIOR FILING DATE: 2001-05-09
 PRIOR APPLICATION NUMBER: 09/180997
 PRIOR FILING DATE: 1998-11-19
 PRIOR APPLICATION NUMBER: 09/267213
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: 09/380137
 PRIOR FILING DATE: 1999-08-25
 PRIOR APPLICATION NUMBER: 09/380138
 PRIOR FILING DATE: 1999-08-25
 PRIOR APPLICATION NUMBER: 09/403297
 PRIOR FILING DATE: 1999-10-18
 PRIOR APPLICATION NUMBER: 09/423741
 PRIOR FILING DATE: 1999-11-10
 PRIOR APPLICATION NUMBER: 09/709238
 PRIOR FILING DATE: 2000-11-08
 PRIOR APPLICATION NUMBER: 09/802706
 PRIOR FILING DATE: 2001-03-09
 PRIOR APPLICATION NUMBER: 09/872035
 PRIOR FILING DATE: 2001-06-01
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 09/924419
 PRIOR FILING DATE: 2001-08-06
 PRIOR APPLICATION NUMBER: 09/927796
 PRIOR FILING DATE: 2001-08-09
 PRIOR APPLICATION NUMBER: 09/929404
 PRIOR FILING DATE: 2001-08-13
 PRIOR APPLICATION NUMBER: 09/931836
 PRIOR FILING DATE: 2001-08-16
 PRIOR APPLICATION NUMBER: 09/941992
 PRIOR FILING DATE: 2001-08-28
 PRIOR APPLICATION NUMBER: 09/946374
 PRIOR FILING DATE: 2001-09-04
 PRIOR APPLICATION NUMBER: 10/001054
 PRIOR FILING DATE: 2001-11-30
 PRIOR APPLICATION NUMBER: 10/052586
 PRIOR FILING DATE: 2002-01-15
 PRIOR APPLICATION NUMBER: 10/081056
 PRIOR FILING DATE: 2002-02-20
 PRIOR APPLICATION NUMBER: 10/119480
 PRIOR FILING DATE: 2002-04-09

Alignment Scores:
 Pred. No.: 207
 Score: 8.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 1.15%
 DB: 9

Length: 192
 Matches: 8
 Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-09-824-647-16 (1-2095) x US-10-237-535-48 (1-192)

Alignment Scores:	207	Length:	192
Pred. No.:	8.00	Matches:	8
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	1.15%	Gaps:	0
rs.	9		

ms-09-824-647-16 (1-2095) x US-10-237-535-48 (1-192)

794 TCTCCAAGGAGAACGCTACCACGG 817

;; PRIOR APPLICATION NUMBER: 60/138385
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;; PRIOR APPLICATION NUMBER: 60/140653
;; PRIOR FILING DATE: 1999-06-22
;; PRIOR APPLICATION NUMBER: 60/141037
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;; PRIOR APPLICATION NUMBER: 60/144732
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;; PRIOR APPLICATION NUMBER: 60/144758
;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/144790
;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/145228
;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/145698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: 60/146222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: 60/146843
;; PRIOR FILING DATE: 1999-08-03
;; PRIOR APPLICATION NUMBER: 60/148188
;; PRIOR FILING DATE: 1999-08-10
;; PRIOR APPLICATION NUMBER: 60/148513
;; PRIOR FILING DATE: 1999-08-12
;; PRIOR APPLICATION NUMBER: 60/149327
;; PRIOR FILING DATE: 1999-08-17
;; PRIOR APPLICATION NUMBER: 60/149395
;; PRIOR FILING DATE: 1999-08-17
;; PRIOR APPLICATION NUMBER: 60/150114
;; PRIOR FILING DATE: 1999-08-20
;; PRIOR APPLICATION NUMBER: 60/151700
;; PRIOR FILING DATE: 1999-08-31
;; PRIOR APPLICATION NUMBER: 60/151734
;; PRIOR FILING DATE: 1999-08-31
;; PRIOR APPLICATION NUMBER: 60/162506
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;; PRIOR APPLICATION NUMBER: 60/170262
;; PRIOR FILING DATE: 1999-12-09
;; PRIOR APPLICATION NUMBER: 60/177118
;; PRIOR FILING DATE: 2000-01-20
;; PRIOR APPLICATION NUMBER: 60/179851
;; PRIOR FILING DATE: 2000-02-02
;; PRIOR APPLICATION NUMBER: 60/180921
;; PRIOR FILING DATE: 2000-02-08
;; PRIOR APPLICATION NUMBER: 60/187202
;; PRIOR FILING DATE: 2000-03-03
;; PRIOR APPLICATION NUMBER: 60/198587
;; PRIOR FILING DATE: 2000-04-18
;; PRIOR APPLICATION NUMBER: 60/199614
;; PRIOR FILING DATE: 2000-04-25
;; PRIOR APPLICATION NUMBER: 60/206330
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/206368
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/209832
;; PRIOR FILING DATE: 2000-06-05
;; PRIOR APPLICATION NUMBER: 60/218371
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;; PRIOR APPLICATION NUMBER: 60/235147
;; PRIOR FILING DATE: 2000-09-22
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;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/380138
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;; PRIOR APPLICATION NUMBER: 09/709238
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;; PRIOR FILING DATE: 2001-06-01
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;; PRIOR APPLICATION NUMBER: 09/929404
;; PRIOR FILING DATE: 2001-08-13
;; PRIOR APPLICATION NUMBER: 09/931836
;; PRIOR FILING DATE: 2001-08-16
;; PRIOR APPLICATION NUMBER: 09/941992
;; PRIOR FILING DATE: 2001-08-28
;; PRIOR APPLICATION NUMBER: 09/946374
;; PRIOR FILING DATE: 2001-09-04
;; PRIOR APPLICATION NUMBER: 10/001054
;; PRIOR FILING DATE: 2001-11-30
;; PRIOR APPLICATION NUMBER: 10/052586
;; PRIOR FILING DATE: 2002-01-15
;; PRIOR APPLICATION NUMBER: 10/081056
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: 10/119480
;; PRIOR FILING DATE: 2002-04-09

Alignment Scores:

Pred. No.:	207	Length:	192
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.15%	Indels:	0
DB:	9	Gaps:	0

US-09-824-647-16 (1-2095) x US-10-238-183-48 (1-192)

QY 794 TCTCCAAGGAGACGTACCACGG 817

Db 2 SerProArgThrLeuProArg 9

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RESULT 44
US-10-238-283-48
; Sequence 48, Application US/10238283
; Publication No. US20030073190A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C15
; CURRENT APPLICATION NUMBER: US/10/238,283
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 48
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-238-283-48

Alignment Scores:
Pred. No.: 207 Length: 192
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-10-238-283-48 (1-192)
QY 794 TCTCAGGAGACGCTACCACGG 817
Db 2 SerProArgThrLeuProArg 9

Search completed: July 7, 2003, 16:04:38
Job time : 104 secs

RESULT 45
US-10-238-370-48
; Sequence 48, Application US/10238370
; Publication No. US20030073191A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C15
; CURRENT APPLICATION NUMBER: US/10/238,283
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 48
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-238-283-48

Alignment Scores:
Pred. No.: 207 Length: 192
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-10-238-283-48 (1-192)
QY 794 TCTCAGGAGACGCTACCACGG 817
Db 2 SerProArgThrLeuProArg 9

Search completed: July 7, 2003, 16:04:38
Job time : 104 secs
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APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C10
; CURRENT APPLICATION NUMBER: US/10/238,370
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 48
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-238-370-48

Alignment Scores:
Pred. No.: 207 Length: 192
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-10-238-370-48 (1-192)
QY 794 TCTCAGGAGACGCTACCACGG 817
Db 2 SerProArgThrLeuProArg 9

Search completed: July 7, 2003, 16:04:38
Job time : 104 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic : protein search, using frame_plus_n2p model

Run on: July 7, 2003, 15:47:40 ; Search time 64.5 Seconds
(without alignments)
6245.011 Million cell updates/sec

Title: US-09-824-647-16

Perfect score: 694

Sequence: 1 cgcagcagaccatggac.....ataaagtgtgcaattttt 2095

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283224 seqs, 96134422 residues

Word size: 1

Total number of hits satisfying chosen parameters: 565536

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-Q/cgn2_1/USPTO.spool/US09824647/runat_07072003.154719.26049/app.query.fasta_1.2247
-DB=PIR_73 -OPM=fastan -SUFFIX=std.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=45 -MODE=LOCAL -OUTFMT=ptp
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09824647.ecgn_1_1108.erunat_07072003.154719.26049 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database: PIR_73.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	405	58.5	593	1 GYHU	granulin precursor
2	32	4.6	589	2 C38128	epithelin/granulin
3	32	4.6	589	2 B38128	epithelin/granulin
4	26	3.7	591	2 I48141	acroganin - guine
5	9	1.3	46	2 A44794	antimicrobial pept
6	9	1.3	633	2 S75525	sensory transducti
7	9	1.3	1191	2 T13850	gene u-shaped prot
8	8	1.2	71	2 C32986	variant surface gl
9	8	1.2	93	2 E25161	hypothetical prote
10	8	1.2	115	2 S07326	variant surface gl
11	8	1.2	135	2 H64481	hypothetical prote
12	8	1.2	143	2 E83560	hypothetical prote
13	8	1.2	150	2 T15585	hypothetical prote
14	8	1.2	171	2 E71530	hypothetical prote

15	8	1.2	178	2 A81687	conserved hypothet
16	8	1.2	181	2 T08793	hypothetical prote
17	8	1.2	188	2 S09789	hypothetical prote
18	8	1.2	193	2 A40738	surface antigen CD
19	8	1.2	229	1 F75267	probable cytochrom
20	8	1.2	245	2 F44490	retrovirus-related
21	8	1.2	253	2 C75611	transcription regu
22	8	1.2	256	2 H82525	uracil-DNA glycosy
23	8	1.2	256	2 T28695	hypothetical prote
24	8	1.2	259	2 S55884	CCHH finger protei
25	8	1.2	260	2 B96866	probable C2H2-type
26	8	1.2	262	2 T06600	acetyl-CoA carboxy
27	8	1.2	271	2 AC3527	aldehyde dehydroge
28	8	1.2	277	2 I52825	gene MAC25 protein
29	8	1.2	282	2 S50031	prostaticin-stimu
30	8	1.2	293	2 A83299	hypothetical prote
31	8	1.2	293	2 T31146	probable DNA inver
32	8	1.2	295	2 F83139	geranyltransfers
33	8	1.2	318	2 E87929	protein T2H2.6 [I
34	8	1.2	334	2 AH3282	primosomal protein
35	8	1.2	345	2 T25138	hypothetical prote
36	8	1.2	358	2 T25137	hypothetical prote
37	8	1.2	361	1 S74694	6-phosphofructokin
38	8	1.2	374	2 AC0972	lipopolysaccharide
39	8	1.2	387	2 H96652	protein F23N19.17
40	8	1.2	394	2 G69230	endo-1,4-beta-gluc
41	8	1.2	434	2 C95163	NOL1/NOP2/sun fami
42	8	1.2	442	2 H98243	agae protein (limp
43	8	1.2	442	2 AD3042	oxaloductase Atu
44	8	1.2	461	2 T43394	potassium channel
45	8	1.2	467	1 VMUT7R	variant surface gl

ALIGNMENTS

RESULT 1

GYHU
granulin precursor [validated] - human
N;Alternate names: epithelin
N;Contains: granulin A; granulin B; granulin C; granulin D; granulin E; granulin F
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1992 #sequence revision 03-May-1996 #text change 08-Dec-2000
C;Accession: JCI284; A38128; A38118; A36698; B36698; C36698; A56873
R;Bandari, V.; Bateman, A.
Biochem. Biophys. Res. Commun. 188, 57-63, 1992
A;Title: Structure and chromosomal location of the human granulin gene.
A;Reference number: JCI284; MUID:93038704; PMID:1417868
A;Accession: JCI284
A;Molecule type: DNA
A;Residues: 1-593 <BHA>
R;Plowman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Todar
J. Biol. Chem. 267, 13073-13078, 1992
A;Title: The epithelin precursor encodes two proteins with opposing activities on
A;Reference number: A38128; MUID:92317004; PMID:1618805
A;Accession: A38128
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-593 <PLO>
A;Cross-references: GB:X62320; NID:931192; PIDN:CRA44196.1; PID:g31193
R;Bandari, V.; Palfree, R.G.E.; Bateman, A.
Proc. Natl. Acad. Sci. U.S.A. 89, 1715-1719, 1992
A;Title: Isolation and sequence of the granulin precursor cDNA from human bone mar
A;Reference number: A38118; MUID:92179253; PMID:1542665
A;Accession: A38118
A;Molecule type: mRNA
A;Residues: 1-406, 'R', 408-433, 'G', 435-453, 'G', 455-459, 'Q', 461-546, 'A', 548-566, 'R',
A;Cross-references: GB:M75161; NID:9183612; PIDN:AA58617.1; PID:g183613
R;Bateman, A.; Belcourt, D.; Bennett, H.; Lazure, C.; Solomon, S.
Biochem. Biophys. Res. Commun. 173, 1161-1168, 1990
A;Title: Granulins, a novel class of peptide from leukocytes.
A;Reference number: A36698; MUID:91097544; PMID:2268320
A;Accession: A36698

J. Biol. Chem. 267, 13073-13078, 1992

A:Title: The epithelin precursor encodes two proteins with opposing activities on epithelium
A:Reference number: A38128; MUID:92317004; PMID:1618805
A:Accession: C38128
A:Molecule type: protein
A:Residues: 1-589 <P>
A:Cross-references: GB:X62321; NID:g50851; PIDN:CAA44197.1; PID:g50852
R:Baba, T.; Nemoto, H.; Watanabe, K.; Arai, Y.; Gerton, G.L.
FEBS Lett. 322, 89-94, 1993
A:Title: Exon/intron organization of the gene encoding the mouse epithelin/granulin precursor
A:Reference number: S32503; MUID:93245991; PMID:8482392
A:Accession: S32503
A:Molecule type: DNA
A:Residues: 18-349, 'L', 351-589 <BAB>
R:Baba, T.; Hoff, H.B.; 351-589 <BAB>
Mol. Reprod. Dev. 34, 233-243, 1993
A:Title: Acrogranin, an acrosomal cysteine-rich glycoprotein, is the precursor of the granulin
A:Reference number: I48141; MUID:93228994; PMID:8471244
A:Accession: I48141
A:Molecule type: protein
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-250, 'L', 252-253, 'V', 255-349, 'L', 351-401, 'SA', 404-589 <RES>
A:Cross-references: GB:M86736; NID:g191766; PIDN:AAA37191.1; PID:g191767
R:Zhou, J.; Gao, G.; Crabb, J.W.; Serrero, G.
J. Biol. Chem. 268, 10863-10869, 1993
A:Title: Purification of an autocrine growth factor homologous with mouse epithelin precursor
A:Reference number: A46705; MUID:93266526; PMID:8496151
A:Accession: A46705
A:Status: preliminary
A:Molecule type: protein
A:Residues: 18-19, 'X', 21-25, 'X', 27-29, 'XX', 32, 'XXX', 119-127:152-154, 'DXK', 158-161, 'X', 161-162, 'X', 163-164, 'X', 165-166, 'X', 167-168, 'X', 169-170, 'X', 171-172, 'X', 173-174, 'X', 175-176, 'X', 177-178, 'X', 179-180, 'X', 181-182, 'X', 183-184, 'X', 185-186, 'X', 187-188, 'X', 189-190, 'X', 191-192, 'X', 193-194, 'X', 195-196, 'X', 197-198, 'X', 199-200, 'X', 201-202, 'X', 203-204, 'X', 205-206, 'X', 207-208, 'X', 209-210, 'X', 211-212, 'X', 213-214, 'X', 215-216, 'X', 217-218, 'X', 219-220, 'X', 221-222, 'X', 223-224, 'X', 225-226, 'X', 227-228, 'X', 229-230, 'X', 231-232, 'X', 233-234, 'X', 235-236, 'X', 237-238, 'X', 239-240, 'X', 241-242, 'X', 243-244, 'X', 245-246, 'X', 247-248, 'X', 249-250, 'X', 251-252, 'X', 253-254, 'X', 255-256, 'X', 257-258, 'X', 259-260, 'X', 261-262, 'X', 263-264, 'X', 265-266, 'X', 267-268, 'X', 269-270, 'X', 271-272, 'X', 273-274, 'X', 275-276, 'X', 277-278, 'X', 279-280, 'X', 281-282, 'X', 283-284, 'X', 285-286, 'X', 287-288, 'X', 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A44794

antimicrobial peptide enAP-1 - horse (fragment)
C:Species: Equus caballus (domestic horse)
C:Date: 24-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-1995
C:Accession: A44794; A40833
R: Couto, M.A.; Harwig, S.S.; Cullor, J.S.; Hughes, J.P.; Lehrer, R.I.
Infect. Immun. 60, 3065-3071, 1992
A:Title: Identification of enAP-1, an antimicrobial peptide from equine neutrophils.
A:Reference number: A44794; MUID:92347972; PMID:1639474
A:Accession: A44794
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-46 <COD>
A:Experimental source: neutrophils
A:Note: sequence extracted from NCBI backbone (NCBIP:109730)
C:Superfamily: granulin

Alignment Scores:
Pred. No.: 8.89 Length: 46
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.30% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x A44794 (1-46)

QY 1573 TGTGGGGAAGGACACTCTGCATGAT 1599

DB 4 CysGlyGluGlyHisPheCysHisASP 12

RESULT 6

S75525
sensory transduction histidine kinase sll1228 - Synecocystis sp. (strain PCC 6803)
N:Alternate names: protein sll1228
C:Species: Synecocystis sp.

A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S75525

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis
S.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S75525

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-633 <KAN>

A:Cross-references: EMBL:D90911; GB:AB001339; NID:g1653083; PIDN:BAAL8086.1; PID:d101881

A:Note: the nucleotide sequence was submitted to the EMBL data library, June 1996

C:Genetics:

A:Start codon: GTG

C:Superfamily: response regulator homology

C:Keywords: phosphoprotein

F:420-531/Domain: response regulator homology <RRH>

F:468/Binding site: phosphate (Asp) (covalent) #status predicted

Alignment Scores:
Pred. No.: 5.99 Length: 633
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.30% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x S75525 (1-633)

QY 1322 CCCACCCGAGACATCGGCTGTGACC 1348

DB 401 ProThrProGluThrSerAlaValThr 409

RESULT 7

T13850

gene u-shaped protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C:Accession: T13850
R:Haenlin, M.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z17795
A:Accession: T13850
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1191 <HA>
A:Cross-references: EMBL:Y12322; NID:e1169964; PID:e1169965; PIDN:CAA72991.1

C:Genetics:

A:Gene: u-shaped

A:Cross-references: FlyBase:FBgn0003963

A:Function:

A:Description: acts as a transregulator of achaete and scute in the dorsal region of

C:Keywords: zinc finger

Alignment Scores:
Pred. No.: 5.45 Length: 1191
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.31% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x T13850 (1-1191)

QY 138 GCAGCAGCTAGCTGGCTCTCCGGG 112

DB 679 AlaAlaAlaValAlaGlySerSerGly 687

RESULT 8

C32986

variant surface glycoprotein 20 Bc1 RF2 - Trypanosoma equiperdum (fragment)
C:Species: Trypanosoma equiperdum

C:Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 26-May-2000

C:Accession: C32986

R:Thon, G.; Baltz, T.; Eisen, H.

Genes Dev. 3, 1247-1254, 1989

A:Title: Antigenic diversity by the recombination of pseudogenes.

A:Reference number: A32986; MUID:90006746; PMID:2792762

A:Accession: C32986

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-71 <THO>

A:Cross-references: GB:X17158

C:Superfamily: variant surface glycoprotein

C:Keywords: glycoprotein

Alignment Scores:
Pred. No.: 84.9 Length: 71
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x C32986 (1-71)

QY 1632 GCCCTGCTCGTGTCTCGGCGACA 1609

DB 58 AlaLeuSerValValSerAlaAla 65

RESULT 9

E25161

hypothetical protein trak - Salmonella typhimurium plasmid PED208 (fragment)

C:Species: Salmonella typhimurium

C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 30-Sep-1993

C:Accession: E25161

R:Finlay, B.B.; Frost, L.S.; Paranchych, W.

J. Bacteriol. 168, 990-998, 1986

A:Title: Nucleotide sequence of the trxALE region from IncFV plasmid pED208.

A:Reference number: A91828; MUID:87056998; PMID:2877970

A:Accession: E25161

A:Molecule type: DNA

A:Residues: 1-93 <PIN>

C:Genetics:

A:Gene: trxA

A:Genome: plasmid

Alignment Scores:
Pred. No.: 81.5 Length: 93
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x E25161 (1-93)

QY 1289 AGTCAGCAGCAGATCTCGCTTCCT 1266

DB 26 SerProAlaThrIleSerLeuPro 33

RESULT 10

S07326

variant surface glycoprotein AnTat 1.8 precursor - Trypanosoma brucei (fragment)

C:Species: Trypanosoma brucei

C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 31-Jan-2000

C:Accession: S07326; A17609

R:Mathysse, G.; Michiels, F.; Hamers, R.; Pays, E.; Steinert, M.

Nature 233, 230-233, 1981

A:Title: Two variant surface glycoproteins of Trypanosoma brucei have a conserved C-term

A:Reference number: A17609; MUID:82013622; PMID:7278981

A:Accession: S07326

A:Molecule type: mRNA

A:Residues: 1-115 <MATH>

A:CROSS-references: EMBL:J01227; NID:gl62397; PIDN:AAA30292.1; PID:gl62398

A:Note: The authors translated the codon GCT for residue 53 as Ser

C:Superfamily: variant surface glycoprotein

C:Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphatid

F.1-92/Product: variant surface glycoprotein (clone AnTat 1.8) (fragment) #status predicted

F.93-115/Domain: carboxyl-terminal propeptide #status predicted <CTP>

F.42/Binding site: carbohydrate (Asn) (covalent) #status predicted

F.92/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asp) (in mature form)

Alignment Scores:
Pred. No.: 79 Length: 115
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x S07326 (1-115)

QY 1632 GCCCTGCTGGTGTCTCGCAGCA 1609

DB 102 AlaLeuSerValValSerAlaAla 109

RESULT 11

H64481

hypothetical protein MJ1457 - Methanococcus jannaschii

C:Species: Methanococcus jannaschii

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C:Accession: H64481

R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,

Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.

son, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Science 273, 1058-1073, 1996

A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C

A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii

A:Reference number: A64300; MUID:96337999; PMID:8686087

A:Accession: H64481

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-135 <BUL>

A:CROSS-references: GB:U67586; GB:L77117; NID:gl592096; PIDN:AAB99470.1; PID:gl592

C:Genetics:

A:Map position: FOR1427020-1427427

A:Start codon: GTG

C:Superfamily: Methanococcus jannaschii hypothetical protein MJ1457

Alignment Scores:
Pred. No.: 77.1 Length: 135
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x H64481 (1-135)

QY 144 GGGACGGCAGCTGTAGCTGGC 121

DB 58 GlyThrAlaAlaAlaValAlaGly 65

RESULT 12

E83560

hypothetical protein PA0679 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: E83560

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: E83560

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-143 <STO>

A:CROSS-references: GB:AE004503; GB:AE004091; NID:g9946553; PIDN:AAG04068.1; GSPDE

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA0679

Alignment Scores:

Pred. No.: 76.4 Length: 143
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x E83560 (1-143)

QY 1458 GCAGCAGCTGCGGATCTCGCA 1435

DB 16 AlaAlaValLeuAlaIleLeuAla 23

RESULT 13

T15585

hypothetical protein C24A3.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T15585

R:Favella, T.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid C24A3.

A:Reference number: Z18373

A:Accession: T15585

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-150 <FAV>

A:Cross-references: EMBL:U40424; NID:gl065542; PID:gl065544; PIDN:AAA81456.1; CESP:C24A3
 C:Genetics:
 A:Gene: CESP:C24A3.5
 A:Introns: 88/3

Alignment Scores:
 Pred. No.: 75.9 Length: 150
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.16% Indels: 0
 DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x T15585 (1-150)

QY 72 GCACCGCTTCAGCCAGCC 49

Db 109 AlaProArgSerHisGlnPro 116

RESULT 14

E71530

hypothetical protein CT303 - Chlamydia trachomatis (serotype D, strain UW3/Cx)

C:Species: Chlamydia trachomatis

C>Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999

C:Accession: E71530

R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998

A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis

A:Reference number: A71570; MUID:9900809; PMID:9784136

A:Accession: E71530

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-171 <ARN>

A:Cross-references: GB:AE001303; GB:AE001273; NID:g3328718; PIDN:AAC67896.1; PID:g332871

A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: CT303

Alignment Scores:

Pred. No.: 74.4 Length: 171
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.15% Indels: 0
 DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x E71530 (1-171)

QY 1125 CTGCTCCCTCCGATACCTGCTG 1148

Db 11 LeuSerLeuLeuArgTyrLeuLeu 18

RESULT 15

A81687

conserved hypothetical protein TC0577 [imported] - Chlamydia muridarum (strain Nigg)

C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn

C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000

C:Accession: A81687

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A:Reference number: A81500; MUID:20150255; PMID:10684935

A:Accession: A81687

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-178 <TFT>

A:Cross-references: GB:AE002326; GB:AE002160; NID:g7190614; PIDN:AAF39412.1; PID:g719061

A:Experimental source: strain Nigg (MoPn)

C:Genetics:

A:Gene: TC0577

Alignment Scores:

Pred. No.: 73.3 Length: 188
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.16% Indels: 0
 DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x S09789 (1-188)

Pred. No.: 73.9 Length: 178
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.15% Indels: 0
 DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x A81687 (1-178)

QY 1125 CTGCTCCCTCCGATACCTGCTG 1148

Db 18 LeuSerLeuLeuArgTyrLeuLeu 25

RESULT 16

T08793

hypothetical protein DKFZp586F0422.1 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999

C:Accession: T08793

R:Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, May 1999

A:Reference number: Z16468

A:Accession: T08793

A:Molecule type: mRNA

A:Residues: 1-181 <KOE>

A:Cross-references: EMBL:AL050173

A:Experimental source: adult uterus; clone DKFZp586F0422

C:Genetics:

A:Note: DKFZp586F0422.1

Alignment Scores:

Pred. No.: 73.8 Length: 181
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.15% Indels: 0
 DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x T08793 (1-181)

QY 1847 TGTGTCAGCCCTCCCTAGACCT 1870

Db 50 SerAlaGlnAlaSerLeuAlaPro 57

RESULT 17

S09789

hypothetical protein UL26 - human cytomegalovirus (strain AD169)

C:Species: human cytomegalovirus, human herpesvirus 5

A:Note: host Homo sapiens (man)

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 21-Jan-2000

C:Accession: S09789

R:Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, M.; Barrell, B.G.

Curr. Top. Microbiol. Immunol. 154, 125-169, 1990

A:Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus

A:Reference number: S09749; MUID:90269039; PMID:2161319

A:Accession: S09789

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-188 <CHE>

A:Cross-references: EMBL:X17403; NID:g59591; PIDN:CAA35425.1; PID:g59631

A:Note: this sequence was submitted to the EMBL Data Library, December 1989

C:Superfamily: human cytomegalovirus hypothetical protein UL26

Alignment Scores:

Pred. No.: 73.3 Length: 188
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.16% Indels: 0
 DB: 2 Gaps: 0

QY 1212 GTGTCGAGCAGCAGCAGCCTC 1189
 |||||
 Db 101 ValValArgAlaAlaSerLeu 108

RESULT 18
 A40738
 surface antigen CD70 - human
 N:Alternate names: CD27-ligand; CD27LG
 C:Species: Homo sapiens (man)
 C:Date: 16-Feb-1994 #sequence_revision 23-Aug-1996 #text_change 05-Nov-1999
 C:Accession: 156214; A40738

R: Bowman, M.R.; Grimmins, M.A.; Yetz-Aldape, J.; Kriz, R.; Kelleher, K.; Herrmann, S.
 J. Immunol. 152, 1756-1761, 1994

A: Title: The cloning of CD70 and its identification as the ligand for CD27.
 A: Reference number: 156214; MUID: 94165470; PMID: 8120384
 A: Accession: 156214
 A: Status: translated from GB/EMBL/DBJ
 A: Molecule type: mRNA
 A: Residues: 1-193 <RES>

R: Goodwin, R.G.; Alderson, M.R.; Smith, C.A.; Ammitage, R.J.; Vandenbos, T.; Jerzy, R.; Grabstein, K.H.; Farrah, T.; Giri, J.G.; Beckmann, M.P.
 Cell 73, 447-456, 1993

A: Title: Molecular and biological characterization of a ligand for CD27 defines a new family of type I membrane proteins.
 A: Reference number: A40738; MUID: 93258810; PMID: 8387892
 A: Accession: A40738
 A: Molecule type: mRNA
 A: Residues: 1-153, V, 155-193 <GOO>

A: Cross-references: GB: S69339; NID: g545772; PIDN: AAB30121.1; PID: g545773
 A: Experimental source: B cells
 A: Note: sequence extracted from NCBI backbone (NCBIN:131664, NCBIP:131665)

C: Geneticks:
 A: Gene: GDB: CD70; CD27LG
 A: Cross-references: GDB: 139157
 A: Map position: 19p13-19p13
 C: Keywords: B-cell; glycoprotein; surface antigen; T-cell; transmembrane protein
 F: 21-38/Domain: transmembrane #status predicted <TMM>
 F: 39-193/Domain: extracellular #status predicted <EXT>
 F: 63,170/Binding site: carbohydrate (Asn) #status predicted

Alignment Scores:
 Pred. No.: 73 Length: 193
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.15% Indels: 0
 DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x A40738 (1-193)

QY 1734 CAGGAGCCCGCGTGGGACGC 1757
 |||||
 Db 76 GlnGlyGlyProAlaLeuGlyArg 83

RESULT 19
 F75267
 Probable cytochrome c4 - Deinococcus radiodurans (strain R1)
 C: Species: Deinococcus radiodurans
 C: Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
 C: Accession: F75267

R: White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Otterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999

A: Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A: Reference number: A75250; MUID: 20036896; PMID: 10567266
 A: Accession: F75267
 A: Status: preliminary
 A: Molecule type: DNA
 A: Residues: 1-229 <WHI>
 A: Cross-references: GB: AE002078; GB: AE000513; NID: g6460306; PIDN: AAF12028.1; PID: g6460306
 A: Experimental source: strain R1

C: Geneticks:
 A: Gene: DR2487
 A: Map position: 1
 C: Superfamily: cytochrome c4; cytochrome c6 homology
 C: Keywords: chromoprotein; duplication; electron transfer; heme; iron; metallopro
 F: 51-122/Domain: cytochrome c6 homology <CYC1>
 F: 146-225/Domain: cytochrome c6 homology <CYC2>
 F: 60-63/Binding site: heme (Cys) (covalent) #status predicted
 F: 64,103/Binding site: heme iron (His, Met) (axial ligands) #status predicted
 F: 157,160/Binding site: heme (Cys) (covalent) #status predicted
 F: 161,206/Binding site: heme iron (His, Met) (axial ligands) #status predicted

Alignment Scores:
 Pred. No.: 71.2 Length: 229
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.15% Indels: 0
 DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x F75267 (1-229)

QY 1370 GCGAACCTGCTGCCGAGCCAGG 1393
 |||||
 Db 133 AlaGluProAlaAlaArgAlaArg 140

RESULT 20
 F44490
 Retrovirus-related reverse transcriptase homolog - Japanese beetle retrotranspos
 C: Species: Popillia japonica (Japanese beetle)
 C: Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
 C: Accession: F44490; A40442
 R: Burke, W.D.; Eickbush, D.G.; Xiong, Y.; Jakubczak, J.; Eickbush, T.H.
 Mol. Biol. Evol. 10, 163-185, 1993

A: Title: Sequence relationship of retrotransposable elements R1 and R2 within and
 A: Reference number: A44490; MUID: 93196484; PMID: 8383793
 A: Contents: retrotransposable element R1
 A: Accession: F44490
 A: Status: preliminary; not compared with conceptual translation
 A: Molecule type: nucleic acid
 A: Residues: 1-245 <BUR>

A: Cross-references: GB: L00944; NID: g160749; PID: g160750
 A: Note: sequence extracted from NCBI backbone (NCBIP:127240)
 R: Jakubczak, J.L.; Burke, W.D.; Eickbush, T.H.
 Proc. Natl. Acad. Sci. U.S.A. 88, 3295-3299, 1991

A: Title: Retrotransposable elements R1 and R2 interrupt the rRNA genes of most in
 A: Reference number: A40442; MUID: 91195337; PMID: 1849649
 A: Accession: A40442
 A: Status: preliminary
 A: Molecule type: DNA
 A: Residues: 173-191 <JAK>

Alignment Scores:
 Pred. No.: 70.5 Length: 245
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.15% Indels: 0
 DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x F44490 (1-245)

QY 1494 CTGCGAAGGAGTGGTCTCTGC 1517
 |||||
 Db 168 LeuArgGluGlySerGlyLeuGly 175

RESULT 21
 C75611
 transcription regulator, IclR family - Deinococcus radiodurans (strain R1)
 C: Species: Deinococcus radiodurans
 C: Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C: Accession: C75611
 R: White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson,

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: C75611
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-253 <WHI>
A:Cross-references: GB:AE001862; GB:AE001825; NID:g6460468; PIDN:AAF12212.1; PID:g646050
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRA0152
A:Map position: 2
C:Superfamily: acetate operon repressor

Alignment Scores: 70.1 Length: 253
Pred. No.: 8.00 Matches: 8
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 1.16% Indels: 0
Query Match: 2 Gaps: 0
DB:

US-09-824-647-16 (1-2095) x C75611 (1-253)

QY 290 CCGATGCCAGCGCTCTGGGAAG 267
DB 135 ProHisAlaThrAlaSerGlyLys 142

RESULT 22
H82525
uracil-DNA glycosylase XF2692 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
R:Accession: H82525
A:Anonymus, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: H82525
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-256 <SIM>
A:Cross-references: GB:AE004075; GB:AE003849; NID:g9107929; PIDN:AAF85489.1; GSPDB:GN001
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laigh
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshuko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

C:Superfamily: uracil-DNA glycosylase

Alignment Scores: 70 Length: 256
Pred. No.: 8.00 Matches: 8
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 1.16% Indels: 0
Query Match: 2 Gaps: 0
DB:

US-09-824-647-16 (1-2095) x H82525 (1-256)
QY 1544 CTACGGCCAGGAGGTGGCAGGC 1521
DB 45 LeuArgAlaArgLysValAlaGly 52

RESULT 23
T28695
hypothetical protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
A:Accession: T28695
R:Parkhill, J.; Bentley, S.D.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1999
A:Reference number: Z20512
A:Accession: T28695
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-256 <PAR>
A:Cross-references: EMBL:AL023496; NID:e1292348; PID:e1292362; PIDN:CAAL8912.1.

Alignment Scores: 70 Length: 256
Pred. No.: 8.00 Matches: 8
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 1.15% Indels: 0
Query Match: 2 Gaps: 0
DB:

US-09-824-647-16 (1-2095) x T28695 (1-256)

QY 308 GCCACGGGCTTCACCTGCAGTG 331
DB 48 AlaHisGlyAlaSerThrAlaVal 55

RESULT 24
S55884
CCHH finger protein 4 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
R:Tague, B.W.; Goodman, H.M.
Plant Mol. Biol. 28, 267-279, 1995
A:Title: Characterization of a family of Arabidopsis zinc finger protein cDNAs.
A:Reference number: S55881; MUID:95322589; PMID:7599312
A:Accession: S55884
A:Molecule type: mRNA
A:Residues: 1-259 <TAG>
A:Cross-references: GB:L39647; NID:g790678; PIDN:AAA87300.1; PID:g790679
C:Genetics:
A:Map position: 1
C:Keywords: DNA binding; zinc finger
F:87-107/Region: zinc finger CCHH motif

Alignment Scores: 69.9 Length: 259
Pred. No.: 8.00 Matches: 8
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 1.16% Indels: 0
Query Match: 2 Gaps: 0
DB:

US-09-824-647-16 (1-2095) x S55884 (1-259)

QY 1269 TCCTCGCTGACACTGCCCTCAGC 1246
DB 55 SerSerLeuThrLeuProLeuSer 62

RESULT 25
B96886
probable C2H2-type zinc finger protein F15E12.19 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: B96686
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.R.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, N.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: B96686
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-260 <STO>
A:Cross-references: GB:AE005173; NID:g11038470; PIDN:AAG27749.1; GSPDB:GN00141
C:Genetics:
A:Gene: F15E12.19
A:Map position: 1

Alignment Scores:
Pred. No.: 69.8 Length: 260
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x B96686 (1-260)

QY 1269 TCCTCGTCGACACTGCCCTCAGC 1246
DB 55 SerSerLeuThrLeuProLeuSer 62

RESULT 26
T06600
acetyl-CoA carboxylase (EC 6.4.1.2), biotin carboxyl carrier chain precursor - soybean
N:Contains: biotin carboxyl carrier chain
C:Species: Glycine max (soybean)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-Jan-2002
C:Accession: T06600
R:Nielsen, N.C.; Reverdatto, S.V.; Beilinson, V.A.
submitted to the EMBL Data Library, November 1995
A:Reference number: Z15788
A:Accession: T06600
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-262 <NIE>
A:Cross-references: EMBL:U40666; NID:g1143318; PIDN:AAB67836.1; PID:g1143319
A:Experimental source: strain Resnik
C:Genetics:
A:Gene: accB-1
A:Genome: nuclear
A:Complex: acetyl-CoA carboxylase is composed of biotin carboxylase (EC 6.3.4.14), carb
C:Function: <ACC>
A:Description: entire acetyl-CoA carboxylase complex catalyzes synthesis of malonyl-CoA
carboxylation of biotin bound to biotin-carboxyl-carrier protein with bicarbonate; carb
A:Pathway: fatty acid biosynthesis
C:Function: <BCC>
A:Description: biotin carboxyl carrier chain is responsible for binding of biotin
A:Pathway: fatty acid biosynthesis
C:Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology
C:Keywords: biotin metabolism; chloroplast; fatty acid biosynthesis; ligase
F:1-47/Domain: transit peptide (chloroplast) #status predicted <TNP>
F:48-262/Product: acetyl-CoA carboxylase, biotin carboxyl carrier chain #status predi

Alignment Scores:
Pred. No.: 69.8 Length: 262
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.16% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x T06600 (1-262)

QY 1404 CCAGCTCCACCCCTGCTCGGCA 1381
DB 161 ProAlaProThrLeuAlaArgAla 168

RESULT 27
AC3527
aldehyde dehydrogenase (NAD) (EC 1.2.1.3) [imported] - Brucella melitensis (strain
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-May-2002
C:Accession: AC3527
R:DelVecchio, V.G.; Kaprat, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Iv
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.;
proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella m
A:Reference number: AD3252; PMID:11756688
A:Accession: AC3527
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-271 <KUR>
A:Cross-references: GB:AE008918; PIDN:AAL53382.1; PID:g17984274; GSPDB:GN00191
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI10141
A:Map position: II
A:Keywords: oxidoreductase

Alignment Scores:
Pred. No.: 69.4 Length: 271
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x AC3527 (1-271)

QY 2021 ACAGGTCCTCCACTCAACGGGAGG 1998
DB 102 ThrGlySerThrGlyThrGlyArg 109

RESULT 28
I52825
gene MAC25 protein - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I52825
R:Murphy, M.; Pykett, M.J.; Harnish, P.; Zang, K.D.; George, D.L.
Cell Growth Differ. 4, 715-722, 1993
A:Title: Identification and characterization of genes differentially expressed in
A:Reference number: I52825; MUID:94059820; PMID:7694637
A:Accession: I52825
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-277 <RES>
A:Cross-references: GB:U19182; NID:g307150; PIDN:AAU16187.1; PID:g307151
C:Genetics:
A:Gene: MAC25
C:Superfamily: Kazal proteinase inhibitor homology
F:104-156/Domain: Kazal proteinase inhibitor homology <KP18>

Alignment Scores:
Pred. No.: 69.2 Length: 277
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 2 Gaps: 0

us-09-824-647-16.std.rpr

Tue Jul 8 07:45:15 2003

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US-09-824-647-16 (1-2095) x I52825 (1-277)
QY 1006 AAGGTACTGTGAACAGGGGCC 1029
DB 153 LysGlyThrCysGluGlnGlyPro 160

RESULT 29
S50031
prostaglandin-stimulating factor - human
C:Species: Homo sapiens (man)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 28-May-1999
R:Yamauchi, T.; Umeda, F.; Masakado, M.; Isaji, M.; Mizushima, S.; Nawata, H.
Biochem. J. 303, 591-598, 1994
A:Title: Purification and molecular cloning of prostaglandin-stimulating factor from serum
A:Reference number: S50031; MUID:95071263; PMID:7980422
A:Accession: S50031
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-282 <YAM>
A:Cross-references: GB:S75725; NID:g861520; PIDN:AB33370.1; PID:g861521
C:Superfamily: Kazal proteinase inhibitor homology
F:104-156/Domain: Kazal proteinase inhibitor homology <KPI8>

Alignment Scores:
Pred. No.: 69 Length: 282
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x S50031 (1-282)
QY 1006 AAGGTACTGTGAACAGGGGCC 1029
DB 153 LysGlyThrCysGluGlnGlyPro 160

RESULT 30
A83299
hypothetical protein PA2778 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: A83299
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B.
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Llin,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: A83299
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-293 <STO>
A:Cross-references: GB:AE004705; GB:AE004091; NID:99948851; PIDN:AG06166.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2778

Alignment Scores:
Pred. No.: 68.6 Length: 293
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x A83299 (1-293)
QY 122 CCAGTACAGCTGCTGCCGCC 145
DB 157 ProLalThrAlaAlaValPro 164

```

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RESULT 31
T31146
probable DNA invertase - Sphingomonas aromaticivorans plasmid pW1
C:Species: Sphingomonas aromaticivorans
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
R:Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.
submitted to the EMBL Data Library, July 1998
A:Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas
A:Reference number: Z20992
A:Accession: T31146
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-293 <ROM>
A:Cross-references: EMBL:AF079317; NID:g3378261; PID:g3378287; PIDN:AA03870.1
C:Genetics:
A:Genome: plasmid pW1
A:Note: orf181

Alignment Scores:
Pred. No.: 68.6 Length: 293
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x T31146 (1-293)
QY 1940 AGATTGAGCCACCTCCATGG 1917
DB 177 ArgLeuArgProHisLeuProTrp 184

RESULT 32
F83139
geranyltransferase PA4043 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F83139
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.;
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: F83139
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-295 <STO>
A:Cross-references: GB:AE004821; GB:AE004091; NID:99950236; PIDN:AG07430.1; GSPDB:
A:Experimental source: strain PA01
C:Genetics:
A:Gene: IS; PA4043

Alignment Scores:
Pred. No.: 68.5 Length: 295
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x F83139 (1-295)
QY 1392 CTGGTCGGCAGCAGGTTCCGCC 1369
DB 144 LeuAlaArgAlaAlaGlySerAla 151

RESULT 33
E87929
protein T22H2.6 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001

```

C:Accession: E87929
 R:Anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes
 A:Reference number: A75000; MUID:95069613; PMID:9851916
 A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.elegans/
 A:Note: Published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 283, 2103, 1999
 A:Accession: E87929
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-318 <STO>
 A:Cross-references: GB:chr_I; PIDN:CA804752.1; PID:93880056; GSPDB:GN00019; CESP:T22H2.6
 C:Genetics:
 A:Gene: T22H2.6
 A:Map position: 1

Alignment Scores:
 Pred. No.: 67.7 Length: 318
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.15% Indels: 0
 DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x E87929 (1-318)

Qy 700 GGCTGCTGCCCAATGCCCAAGCC 723
 Db 79 GlyCysCysPrometProasna1a 86
 |||||

RESULT 34
 AH3282

primosomal protein N' [imported] - Brucella melitensis (strain 16M)
 C:Species: Brucella melitensis
 C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
 C:Accession: AH3282
 R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mijar, C.; Los, T.; Ivanova, N.; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
 A:Reference number: AD3252; PMID:11756688
 A:Accession: AH3282
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-334 <KUR>
 A:Cross-references: GB:AB008917; PIDN:AL51427.1; PID:917982134; GSPDB:GN00190
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BMEI0245
 A:Map position: 1

Alignment Scores:
 Pred. No.: 67.2 Length: 334
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.16% Indels: 0
 DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x AH3282 (1-334)

Qy 531 CAGCTGCAGAGGACCGGTGG 508
 Db 305 GlnValAlaGluGlyThrValArg 312
 |||||

RESULT 35
 T25138

hypothetical protein T22H2.6b - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T25138
 R:Lennard, N.
 submitted to the EMBL Data Library, November 1996

A:Reference number: Z19985

A:Accession: T25138

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-345 <WIL>

A:Cross-references: EMBL:Z81595; PIDN:CA854305.1; GSPDB:GN00019; CESP:T22H2.6b

A:Experimental source: clone T22H2

C:Genetics:

A:Gene: CESP:T22H2.6b

A:Map position: 1

A:Introns: 93/3; 232/3; 314/3

Alignment Scores:

Pred. No.: 66.9 Length: 345
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.15% Indels: 0
 DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x T25138 (1-345)

Qy 700 GGCTGCTGCCCAATGCCCAAGCC 723

Db 119 GlyCysCysPrometProasna1a 126

|||||

RESULT 36

T25137

hypothetical protein T22H2.6a - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T25137

R:Lennard, N.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19985

A:Accession: T25137

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-358 <WIL>

A:Cross-references: EMBL:Z81595; PIDN:CA854304.1; GSPDB:GN00019; CESP:T22H2.6a

A:Experimental source: clone T22H2

C:Genetics:

A:Gene: CESP:T22H2.6a

A:Map position: 1

A:Introns: 93/3; 232/3; 314/3

Alignment Scores:

Pred. No.: 66.6 Length: 358
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.15% Indels: 0
 DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x T25137 (1-358)

Qy 700 GGCTGCTGCCCAATGCCCAAGCC 723

Db 119 GlyCysCysPrometProasna1a 126

|||||

RESULT 37

S74694

6-phosphofructokinase (EC 2.7.1.11) pfkA-2 - Synecocystis sp. (strain PCC 6803)

N:Alternate names: protein sll1196

C:Species: Synecocystis sp.

A:Variety: PCC 6803

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000

C:Accession: S74694

R:Kaneke, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O. K.; Okumura, S.; Shimpou, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecch

submitted to the EMBL Data Library, November 1996

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S74694

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-361 <KAN>

A:Cross-references: EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BAA16845.1; PID:g165191

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Genetics:

A:Gene: pfkA-2

C:Superfamily: 6-phosphofructokinase; 6-phosphofructokinase 1 homology

C:Keywords: glycolysis; phosphotransferase

F:7-313/Domain: 6-phosphofructokinase 1 homology <GPF>

Alignment Scores:
Pred. No.: 66.5 Length: 361
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x S74694 (1-361)

QY 1152 TTGGCAGCAGTATCGGAGGAGG 1129

DB 193 LeuAlaAlaGlyIleGlyGly 200

RESULT 38

AC0972

lipopolysaccharide core biosynthesis protein [imported] - Salmonella enterica subsp. ent

C:Species: Salmonella enterica subsp. enterica serovar Typhi

A:Note: this species has also been called Salmonella typhi

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001

C:Accession: AC0972

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Moule, S.; O'Garra, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero

A:Reference number: AB05002; PMID:11677608

A:Accession: AC0972

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-374 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD03271.1; PID:g16504892; GSPDB:GN00176

C:Genetics:

A:Gene: waag

C:Superfamily: probable hexosyltransferase ytxN

Alignment Scores:
Pred. No.: 66.1 Length: 374
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x AC0972 (1-374)

QY 1125 GCTGCTGACATTATCAGGGGAC 1102

DB 364 AlaAlaAspIleIleThrGlyAsp 371

RESULT 39

H96652

Protein F23N19.17 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C:Accession: H96652

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.

ansen, N.P.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzi

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: AB6141; MUID:21016719; PMID:11130712

A:Accession: H96652

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-387 <STO>

A:Cross-references: GB:AE005173; NID:g6630455; PIDN:AAF19543.1; GSPDB:GN00141

C:Genetics:

A:Gene: F23N19.17

A:Map position: 1

C:Superfamily: aspartate aminotransferase

Alignment Scores:
Pred. No.: 65.8 Length: 387
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x H96652 (1-387)

QY 465 GGGCAGCAGCCCCAGGAGCATC 442

DB 180 GlyAlaAlaProGlyAlaIle 187

RESULT 40

G69230

endo-1,4-beta-glucanase related protein - Methanobacterium thermoautotrophicum (str

C:Species: Methanobacterium thermoautotrophicum

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999

C:Accession: G69230

R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge,

K.; Oiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan

K.; S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H:

A:Reference number: A69000; MUID:98037514; PMID:9371463

A:Accession: G69230

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-394 <MTH>

A:Cross-references: GB:AE000871; GB:AE000666; NID:g2622069; PIDN:AB85473.1; PID:g2

A:Experimental source: strain Delta H

C:Genetics:

A:Gene: MTH977

A:Start codon: TTG

Alignment Scores:
Pred. No.: 65.6 Length: 394
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x G69230 (1-394)

QY 1340 GCTGTGACACACACACAGCTGCC 1363

DB 262 AlaValThrSerThrProAlaAla 269

RESULT 41

C95163

NOL1/NOP2/sun family protein [imported] - Streptococcus pneumoniae (strain TIGR4)

C:Species: Streptococcus pneumoniae

C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

C:Accession: C95163
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
son, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
son, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: C95163
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-434 <KUR>
A:Cross-references: GB:AE005672; PIDN:AAK75500.1; PID:g14972890; GSPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SPI402

Alignment Scores:
Pred. No.: 64.6 Length: 434
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x C95163 (1-434)

OY 371 GAGTTGTACTGATCTTTGGAAG 348
|||||
DB 333 GluLeuLeuProAspLeuTrpLys 340

RESULT 42

H98243
agaE protein [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C:Accession: H98243
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourullo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*
A:Reference number: A97359; PMID:11743194
A:Accession: H98243
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-442 <KUR>
A:Cross-references: GB:AE007870; PIDN:AAK89474.1; PID:g15159342; GSPDB:GN00170
C:Genetics:
A:Gene: AGR_L1801
A:Map position: linear chromosome

Alignment Scores:
Pred. No.: 64.5 Length: 442
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x H98243 (1-442)

OY 1125 GCTGCTGACATTATCAGGGGAC 1102
|||||
DB 409 AlaAlaAspIleIleThrGlyAsp 416

RESULT 43

AD3042
oxidoreductase Atu3952 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C:Accession: AD3042
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, H.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan

; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AD3042
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-442 <KUR>
A:Cross-references: GB:AE008689; PIDN:AA44754.1; PID:g17742390; GSPDB:GN00187
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu3952
A:Map position: linear chromosome

Alignment Scores:
Pred. No.: 64.5 Length: 442
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x AD3042 (1-442)

OY 1125 GCTGCTGACATTATCAGGGGAC 1102
|||||
DB 409 AlaAlaAspIleIleThrGlyAsp 416

RESULT 44

T43394
potassium channel chain n2p18 homolog - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C:Accession: T43394
R:Kunkel, M.T.; Salkoff, L.
submitted to the EMBL Data Library, August 1998
A:Description: Potassium channels in *C. elegans*.
A:Reference number: 222479
A:Accession: T43394
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-461 <KUN>
A:Cross-references: EMBL:AF083650; PIDN:AA32861.1

Alignment Scores:
Pred. No.: 64.1 Length: 461
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x T43394 (1-461)

OY 72 GCACCGGCTCCAGCCACACAGCCC 49
|||||
DB 420 AlaProArgSerSerHisGlnPro 427

RESULT 45

VMTU7R
variant surface glycoprotein 7 precursor - *Trypanosoma brucei rhodesiense* (fragmer
N:Alternate names: metacyclic variable antigen; VSG
C:Species: *Trypanosoma brucei rhodesiense*
C:Date: 28-Feb-1986 #sequence_revision 28-Feb-1986 #text_change 17-Nov-2000
C:Accession: A03393
R:Lenardo, M.J.; Rice-Ficht, A.C.; Kelly, G.; Esser, K.M.; Donelson, J.E.
Proc. Natl. Acad. Sci. U.S.A. 81, 6642-6646, 1984
A:Title: Characterization of the genes specifying two metacyclic variable antigen
A:Reference number: A94011; MUID:85038570; PMID:6593722
A:Accession: A03393
A:Molecule type: mRNA

Tue Jul 8 07:45:15 2003

A: Residues: 1-467 <LEN>
 C: Superfamily: variant surface glycoprotein
 C: Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkage
 F: 1-21/Domain: signal sequence (fragment) #status predicted <SIG>
 F: 28-444/Product: variant surface glycoprotein 7 (fragment) #status predicted <MAT>
 F: 445-467/Domain: carboxyl-terminal propeptide #status predicted <CTP>
 F: 108,252,416/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F: 444/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asp) (in mature form)

Alignment Scores:	63.9	Length:	467
Pred. No.:	8.00	Matches:	8
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	1.16%	Gaps:	0
DB:	1		

US-09-824-647-16 (1-2095) x VMUT7R (1-467)

QY 1632 GCCCTGTCGGTTGTCTCGCAGCA 1609

454 AlaLeuSerValValSerAlaAla 461

Search completed: July 7, 2003, 15:51:20
Job time : 91.5 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: July 7, 2003, 15:47:40 ; Search time 35 Seconds

(without alignments)

4965.309 Million cell updates/sec

Title: US-09-824-647-16

Perfect score: 694

Sequence: 1 ccgaggcagaccatgtggac.....ataaagtgtcactttctt 2095

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 112892 seqs, 41476328 residues

Word size: 1

Total number of hits satisfying chosen parameters: 225614

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-O=/cgn2.1/USPTO.spool/US09824647/runat_07072003.154717_26023/app_query.fasta.1.2247
-DB=SwissProt_40 -QFWT=fastan -SUFFIX=std.rsp -MINMATCH=0.1 -LOOPCL=0
-LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=45 -MODE=LOCAL
-OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09824647.ecgn.1.1.46.erunat_07072003.154717_26023 -NCPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -Fgapop=6
-Fgapext=7 -Ygapop=60 -Ygapext=60 -DELOP=6 -DELEXT=7

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	406	58.5	593	1 GRN_HUMAN	P28799 h granulins
2	32	4.6	588	1 GRN_RAT	P23785 r granulins
3	32	4.6	589	1 GRN_MOUSE	P28798 mus musculus
4	26	3.7	591	1 GRN_CAVPO	P28797 cavia porce
5	9	1.3	46	1 ENAL_HORSE	P80930 equus caball
6	8	1.2	115	1 VSAB_TRYBB	P06017 trypanosoma
7	8	1.2	135	1 YE57_METJA	Q58852 methanococc
8	8	1.2	181	1 CU25_HUMAN	O9Y426 homo sapien
9	8	1.2	188	1 UL26_HCMVA	P16762 human cytom
10	8	1.2	193	1 TNF7_HUMAN	P32970 homo sapien
11	8	1.2	212	1 KTH1_HUMAN	P23919 homo sapien
12	8	1.2	245	1 PO11_POPJA	Q03276 popillia ja
13	8	1.2	262	1 BCCP_SOYBN	Q42783 glycine max
14	8	1.2	269	1 CIT2_MOUSE	Q35740 mus muscul
15	8	1.2	296	1 CRK_XENLA	P87378 xenopus lae
16	8	1.2	334	1 EFBL_CHICK	O73612 gallus gall
17	8	1.2	361	1 K6PE_SYNY3	P72830 synecocyst
18	8	1.2	401	1 NPT4_HUMAN	O00476 homo sapien

c 19	8	1.2	403	1	AAT4_ARATH	P46646 arabidopsis
c 20	8	1.2	447	1	RRA_FUGRU	Q9W523 fugu rubrip
c 21	8	1.2	467	1	VSG7_TRYBR	P02898 trypanosoma
c 22	8	1.2	488	1	DGT1_HUMAN	O75907 homo sapien
c 23	8	1.2	491	1	DGT1_CERAE	O9gmfl cercopithec
c 24	8	1.2	502	1	UAP1_ARATH	O64765 arabidopsis
c 25	8	1.2	503	1	VSAL_TRYBB	P06015 trypanosoma
c 26	8	1.2	503	1	VS16_TRYBB	P06014 trypanosoma
c 27	8	1.2	516	1	YCP7_BRAJA	Q45221 bradyrhizob
c 28	8	1.2	532	1	VS13_TRYBB	P26328 trypanosoma
c 29	8	1.2	561	1	EST3_RAT	P26328 trypanosoma
c 30	8	1.2	562	1	ES22_MOUSE	O64176 mus musculu
c 31	8	1.2	572	1	ALAD_HUMAN	P23100 homo sapien
c 32	8	1.2	629	1	YS50_MYCTU	O05809 mycobacteri
c 33	8	1.2	671	1	ALYS_ENTFA	P37710 enterococc
c 34	8	1.2	678	1	T2D5_RAT	O63801 rattus norv
c 35	8	1.2	693	1	ROXN_HUMAN	O9ugr2 homo sapien
c 36	8	1.2	3672	1	LML2_CAEEL	Q21313 caenorhabdi
c 37	7	1.0	37	1	SMS_PETMA	P21779 petromyzon
c 38	7	1.0	57	1	6H9A_HUMAN	Q13653 homo sapien
c 39	7	1.0	73	1	RS27_METKA	O8ty87 methanopyru
c 40	7	1.0	96	1	EXOX_RHISN	P14185 rhizobium s
c 41	7	1.0	111	1	SSIX_STRHY	O95641 streptomyce
c 42	7	1.0	112	1	CLP3_DROME	P07188 drosophila
c 43	7	1.0	113	1	GV12_HALN1	Q9hht7 halobacteri
c 44	7	1.0	115	1	MOT1_BOVIN	O62820 bos taurus
c 45	7	1.0	115	1	YDG5_SCHPO	Q10493 schizosacch

ALIGNMENTS

RESULT 1

GRN_HUMAN	STANDARD:	PRT:	593 AA.
AC P28799; P23781; P23782; P23783; P23784; Q9BWE7;			
DT 01-NOV-1991 (Rel. 20, Created)			
DT 01-DEC-1992 (Rel. 24, Last sequence update)			
DT 15-JUN-2002 (Rel. 41, Last annotation update)			
DE Granulins precursor (Acrogranin) [Contains: Paragranulin; Granulin 1			
DE (Granulin G); Granulin 2 (Granulin F); Granulin 3 (Granulin B);			
DE Granulin 4 (Granulin A); Granulin 5 (Granulin C); Granulin 6 (Granulin			
DE D); Granulin 7 (Granulin E)]			
GN GRN			
OS Homo sapiens (Human)			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RC TISSUE=Bone marrow;			
RX MEDLINE=92179253; PubMed=1542665;			
RA Bhandari V., Palfree R.G.E., Bateman A.;			
RT "Isolation and sequence of the granulin precursor cDNA from human			
RL bone marrow reveals tandem cysteine-rich granulin domains.";			
RL Proc. Natl. Acad. Sci. U.S.A. 89:1715-1719(1992).			
RN [2]			
RP REVISIONS, SEQUENCE FROM N.A.			
RX MEDLINE=93038704; PubMed=1417868;			
RA Bhandari V., Bateman A.;			
RT "Structure and chromosomal location of the human granulin gene.";			
RL Biochem. Biophys. Res. Commun. 188:57-63(1992).			
RN [3]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Kidney;			
RX MEDLINE=92317004; PubMed=1618805;			
RA Plowman G.D., Green I.M., Neubauer M.G., Buckley S.D., McDonald V.L.,			
RA Todaro G.J., Shoyab M.;			
RT "The epithelial precursor encodes two proteins with opposing activities			
RL on epithelial cell growth.";			
RL J. Biol. Chem. 267:13073-13078(1992).			
RN [4]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Brain;			

RA Yu W., Gibbs R.A.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
[5]
RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RP TISSUE-Cervix, and Lung;
RC Strausberg R.;
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL [6]
RN SEQUENCE OF 206-233; 281-336; 364-396 AND 442-447.
RP TISSUE-Leukocyte;
RC MEDLINE=91097544; PubMed=2268320;
RA Bateman A., Belcourt D.R., Bennett H.P., Lazure C., Solomon S.;
RT "Granulins, a novel class of peptide from leukocytes";
RL Biochem. Biophys. Res. Commun. 173:1161-1168(1990).
CC -!- FUNCTION: GRANULINS HAVE POSSIBLE CITOKINE-LIKE ACTIVITY. THEY MAY
CC PLAY A ROLE IN INFLAMMATION, WOUND REPAIR, AND TISSUE REMODELING.
CC -!- FUNCTION: GRANULIN A PROMOTES PROLIFERATION OF THE EPITHELIAL
CC CELL LINE A431 IN CULTURE WHILE GRANULIN B ACTS AS AN ANTAGONIST
CC TO GRANULIN A, INHIBITING THE GROWTH.
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be
CC produced by alternative splicing.
CC -!- TISSUE SPECIFICITY: IN MYELOGENOUS LEUKEMIC CELL LINES OF
CC PROMONOCYTIC, PROMYELOCYTIC, AND PROERYTHROID LINEAGE, IN
CC FIBROBLASTS, AND VERY STRONGLY IN EPITHELIAL CELL LINES. PRESENT
CC IN INFLAMMATORY CELLS AND BONE MARROW. HIGHEST LEVELS IN KIDNEY.
CC -!- PTM: GRANULINS ARE DISULFIDE BRIDGED.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M75161; AAA58617.1; ALT_SEQ.
DR EMBL; X62320; CAA44196.1; .
DR EMBL; AF055008; AAC09359.1; .
DR EMBL; BC000324; AAH00324.1; .
DR EMBL; BC010577; AAH10577.1; .
DR PIR; A38118; GYHU.
DR PIR; D36698; D36698.
DR PIR; JC1284; JC1284.
DR Genew; HGNC:4601; GRN.
DR MIM; 138945; .
DR InterPro; IPR000118; Granulin.
DR Pfam; PF00396; granulin; 7.
DR SMART; SM00277; GRAN; 7.
DR PROSITE; PS00799; GRANULINS; 7.
KW Cytokine; Repeat; Glycoprotein; Signal; Alternative splicing;
KW Polymorphism.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 593 ACROGRANIN.
FT PEPTIDE 18 747 PARAGRANULIN.
FT PEPTIDE 258 7113 GRANULIN 1.
FT PEPTIDE 7123 7179 GRANULIN 2.
FT PEPTIDE 206 261 GRANULIN 3.
FT PEPTIDE 281 336 GRANULIN 4.
FT PEPTIDE 364 7417 GRANULIN 5.
FT PEPTIDE 442 7496 GRANULIN 6.
FT PEPTIDE 7518 7573 GRANULIN 7.
FT CARBOHYD 118 118 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 236 236 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 265 265 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 368 368 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 530 530 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 377 531 MISSING (IN ISOFORM 2).
FT VARIANT 454 454 G -> O.
FT /FTID=VAR_003445.
FT CONFLICT 219 219 S -> H (IN REF. 6).
FT CONFLICT 386 386 W -> H (IN REF. 6).
FT SEQUENCE 593 AA; 63473 MW; 4E402BDB16DE2819 CRC64;
SQ

Alignment Scores:
Pred. No.: 0 Length: 593
Score: 406.00 Matches: 406
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 58.50% Indels: 0
DB: 1 Gaps: 0
US-09-824-647-16. (1-2095) x GRN_HUMAN (1-593)
QY 13 ATGTGGACCTGTGGAGCTGGTGGCTTAACACAGCGGTGTGGTGGACCGGTGC 72
DB 1 MetTrpThrLeuValSerTrpValAlaLeuThrAlaGlyLeuValAlaGlyThrArgCys 20
QY 73 CCAGATGGTCAGTTCTGCTGCTGTGGCTGTGGACCCCGGAGGAGCCAGGTACAGC 132
DB 21 ProAspGlyGlnPheCysProValAlaCysCysLeuAspProGlyGlyAlaSerTyrSer 40
QY 133 TGTGCGCTGCTCCCTTCTGGACAAATGGCCCAACACTGACGACGATCTGGTGGCCCC 192
DB 41 CysCysArgProLeuLeuAspLysTrpProThrThrLeuSerArgHisLeuGlyCysPro 60
QY 193 TGCAGGTTATGCTCCACTGCTGTGGCGCCACTCTCTCATCTTTACCTCTCAGGGACT 252
DB 61 CysGlnValAspAlaHisCysSerAlaGlyHisSerCysIlePheThrValSerGlyThr 80
QY 253 TCCAGTTGCTGCTCCCTCCAGAGCGCTGGCGGATGGCGGATGGCCATCTGCTGCCCA 312
DB 81 SerSerCysCysProPheProGluAlaValAlaCysGlyAspGlyHisHisCysCysPro 100
QY 313 CGGGCTTCCACTGAGTCAGTCAGAGCGGGGATGCTCTCCAAAGATCAGGTAACTCC 372
DB 101 ArgGlyPheHisCysSerAlaAspGlyArgSerCysPheGlnArgSerGlyAsnAsnSer 120
QY 373 GTGGTGCATCCAGTGCCTGATAGTCAGTTCGAATGCCGAGACTTCTCCACGTGCTGT 432
DB 121 ValGlyAlaIleGlnCysProAspSerGlnPheGluCysProAspPheSerThrCysCys 140
QY 433 GTTATGGTCAGTGGCTCTCGGGGTGCTGCCCATGCTGCCAGCTTCTGCTGTGAGAC 492
DB 141 ValMetValAspGlySerTrpGlyCysCysProMetProGlnAlaSerCysCysGluAsp 160
QY 493 AGGTGTCAGTGTCTCCGACCGTCTCTGGACCTGTTCGGACCTGTCACACCGCTGCATCA 552
DB 161 ArgValHisCysCysProHisGlyAlaPheCysAspLeuValHisThrArgCysIleThr 180
QY 553 CCCAGCGGCACCCACCCCTGCAAGAAGCTCCCTGCCACAGAGGACTAACAGGCGAGTG 612
DB 181 ProThrGlyThrHisProLeuAlaLysLysLeuProAlaGlnArgThrAsnArgAlaVal 200
QY 613 GCCTTGTCCAGCTCGGTTCATGTCTCGGACGACGCTCCCGGTGCTGATGGTTCTTACC 672
DB 201 AlaLeuSerSerSerValMetCysProAspAlaArgSerArgCysProAspGlySerThr 220
QY 673 TGTGTGAGCTGCCAGTGGAGAGTATGCTGCTGCCAATGCCCAATGCCCACTGCTGC 732
DB 221 CysCysGluLeuProSerGlyLysTyrGlyCysCysProMetProAsnAlaThrCysCys 240
QY 733 TCCGATCACTGCACCTGCTGCCCGCCCAAGACACTGTGTGACCTGATCAGAGTAAGTGC 792
DB 241 SerAspHisLeuHisCysCysProGlnAspThrValCysAspLeuIleGlnSerLysCys 260
QY 793 CTCTCCAAGGAGAACCTACCGGACCTCTCTCACTAAGTGTGCTGCTGGCGCACACAGTGGGC 852
DB 261 LeuSerLysGluAsnAlaThrThrAspLeuLeuThrLysLeuProAlaHisThrValGly 280
QY 853 GATGTGAATGTGACATGAGGTGAGGTGAGCTGCCAGATGGCTATACCTGCTGCTCCCTCTACAG 912
DB 281 AspValLysCysAspMetGluValSerCysProAspGlyTyrThrCysCysArgLeuGln 300
QY 913 TCGGGGCGCTGGGCTGCTGCCCTTTTACCCAGCGCTGTGTGCTGTGAGGACCATACAC 972
DB 301 SerGlyAlaTrpGlyCysCysProPheThrGlnAlaValCysCysGluAspHisIleHis 320


```

01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Granulins precursor (Acrogranin) [contains: Granulin 1; Granulin 2;
Granulin 3; Granulin 4; Granulin 5; Granulin 6; Granulin 7]
(Fragment).
GRN.
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Mystricognathi; Caviidae; Cavia.
NCBI_TaxID=10141;
[1]
SEQUENCE FROM N.A., AND SEQUENCE OF 4-21.
TISSUE=Testis;
MEDLINE=93228994; PubMed=8471244;
Baba T., Hoff H.B. III, Nemoto H., Lee H., Orth J., Arai Y.,
Gerton G.L.;
"Acrogranin, an acrosomal cysteine-rich glycoprotein, is the
precursor of the growth-modulating peptides, granulins, and
epithelins, and is expressed in somatic as well as male germ cells.";
Mol. Reprod. Dev. 34:233-243(1993).
-!- FUNCTION: GRANULINS HAVE POSSIBLE CYTOKINE-LIKE ACTIVITY. THEY MAY
PLAY A ROLE IN INFLAMMATION, WOUND REPAIR, AND TISSUE REMODELING.
-!- TISSUE SPECIFICITY: UBIQUITOUS.
-!- PTM: GRANULINS ARE DISULFIDE BRIDGED.
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-----
EMBL; M86735; AAA37030.1; -.
InterPro: IPR000118; Granulin.
DR Pfam; PF003396; granulin; 7.
DR SMART; SM00277; GRAN; 6.
DR PROSITE; PS00799; GRANULINS; 6.
DR Cytokine; Repeat; Signal; Glycoprotein.
FT FT NON_TER 1 1
FT FT SIGNAL <1 3
FT FT CHAIN 4 591 ACROGRANIN.
FT FT PEPTIDE 253 298 GRANULIN 1.
FT FT PEPTIDE 7111 7164 GRANULIN 2.
FT FT PEPTIDE 206 261 GRANULIN 3.
FT FT PEPTIDE 281 335 GRANULIN 4.
FT FT PEPTIDE 7376 7415 GRANULIN 5.
FT FT PEPTIDE 439 2494 GRANULIN 6.
FT FT PEPTIDE 7518 7569 GRANULIN 7.
FT FT CARBOHYD 183 183 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 591 AA; 62586 MW; EE79CF8F21CB8A1 CRC64;
-----
Alignment Scores:
Pred. No.: 1.05e-16 Length: 591
Score: 26.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: Indels: 0
DB: Gaps: 0
-----
US-09-824-647-16 (1-2095) x GRN_CAVPO (1-591)
Qy 442 GATGGCTCTGGGGGTGCTGCCCATGCCCGAGGCTTCCTGCTGTGACAGAGGTGCAC 501
Db 130 AspGlySerTrpGlyCysCysProMetProGlnAlaSerCysCysGluAspArgValHis 149
Qy 502 TGCTGTCCGCACGGTGCC 519
Db 150 CysCysProHisGlyAla 155
-----
RESULT 5
ENAL_HORSE

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ID ENAL_HORSE STANDARD; PRT; 46 AA.
AC P06017;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE Antimicrobial peptide enAP-1 (Fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE
RC TISSUE=Neutrophils;
RX MEDLINE=92347972; PubMed=1639474;
RA Couto A.M., Harwig S.S.L., Cullor J.S., Hughes J.P., Lehrer R.I.;
RT "Identification of enAP-1, an antimicrobial peptide from equine
RT neutrophils."
RL Infect. Immun. 60:3065-3071(1992).
CC -1- FUNCTION: HAS ANTIMICROBIAL ACTIVITY AGAINST GRAM-NEGATIVE AND
CC GRAM-POSITIVE BACTERIA.
CC -1- SIMILARITY: SEEMS TO CORRESPONDS TO GRANULIN 7.
DR InterPro: IPR000118; Granulin.
DR Pfam: PF003396; granulin; 1.
DR SMART: SM00277; GRAN; 1.
DR PROSITE: PS00799; GRANULINS; PARTIAL.
KW Antibiotic.
FT NON_TER 46 46
SQ SEQUENCE 46 AA; 4888 MW; 2171934C15265862 CRC64;

Alignment Scores:
Pred. No.: 5.92 Length: 46
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.30% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x ENAL_HORSE (1-46)
QY 1573 TGRGGGAAGGACACTCTGCCATGAT 1599
|||||
DB 4 CysGlyGluGlyHisPheCysHisAsp 12

RESULT 6
VSAS_TRYBB STANDARD; PRT; 115 AA.
ID VSAS_TRYBB
AC P06017;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 01-MAY-1992 (Rel. 22, Last annotation update)
DE Variant surface glycoprotein ANTAT 1.8 (VSG) (Fragment).
OS Trypanosoma brucei brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82013622; PubMed=7278981;
RA Matthysens G., Michiels F., Hamers R., Pays E., Steinert M.;
RT "Two variant surface glycoproteins of Trypanosoma brucei have a
RT conserved C-terminus."
RL Nature 293:230-233(1991).
CC -1- FUNCTION: VSG FORMS A COAT ON THE SURFACE OF THE PARASITE. THE
CC TYPANOSOME EVADES THE IMMUNE RESPONSE OF THE HOST BY EXPRESSING
CC A SERIES OF ANTIGENICALLY DISTINCT VSGS FROM AN ESTIMATED 1000
CC VSG GENES.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC A SOLUBLE FORM IS RELEASED FROM RUPTURED CELLS BY THE ACTION OF A
CC PI-PLC.
CC
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CC
CC ENBL; U67586; AAB99470.1; -
DR TIGR; MJ1457; -
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 11 31
FT TRANSMEM 57 77
SQ SEQUENCE 135 AA; 14508 MW; E69A4F18B630A92D CRC64;

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CC
CC ENBL; J01227; AAA30292.1; -
DR PIR; S07326; S07326.
DR InterPro: IPR001812; Trypan-glycop.
DR Pfam: PF00913; Trypan-glycop; 1.
KW Glycoprotein; Antigen; Trypanosomiasis; GPI-anchor; Membrane.
FT NON_TER 1 1
FT CHAIN 1 <1 92 VARIANT SURFACE GLYCOPROTEIN ANTAT 1.8.
FT PROPEP 93 115 HYDROPHOBIC, REMOVED DURING MATURATION.
FT LIPID 92 92 GPI-ANCHOR.
SQ SEQUENCE 115 AA; 12530 MW; 12761F33D1305C7E CRC64;

Alignment Scores:
Pred. No.: 48.5 Length: 115
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x VSAS_TRYBB (1-115)
QY 1632 GCCCTGCTGGTGTCTCGGCAGCA 1609
|||||
DB 102 AlaLeuSerValValSerAlaAla 109

RESULT 7
YES7_METJA STANDARD; PRT; 135 AA.
ID YES7_METJA
AC Q58852;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ1457.
GN MJ1457.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcales; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC
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CC
CC ENBL; U67586; AAB99470.1; -
DR TIGR; MJ1457; -
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 11 31
FT TRANSMEM 57 77
SQ SEQUENCE 135 AA; 14508 MW; E69A4F18B630A92D CRC64;
```


Alignment Scores:
 Pred. No.: 47.3 Length: 135
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.16% Indels: 0
 DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x YE57_METJA (1-135)

QY 144 GGGACGGCAGCGCTGTAGCTGGC 121

Db 58 GlyThrAlaAlaAlaValAlaGly 65

RESULT 8

CU25_HUMAN STANDARD; PRT; 181 AA.

AC Q9Y426;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Hypothetical protein C21orf25 (Fragment).

GN C21ORF25.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Uterus;

RA Koehler K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemann S.;

RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

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CC EMBL; AL050173; CAB43307.1;

DR Genew; HGNC:1266; C21orf25.

KW Hypothetical protein.

FT NON_TER

SQ SEQUENCE 181 AA; 1799 MW; 9F4831DCEB7DF2A CRC64;

Alignment Scores:
 Pred. No.: 45.2 Length: 181
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.15% Indels: 0
 DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x CU25_HUMAN (1-181)

QY 1847 TCTCTCAGGCTCCCTAGCACCT 1870

Db 50 SerAlaGlnAlaSerLeuAlaPro 57

RESULT 9

UL26_HCMVA

ID UL26_HCMVA STANDARD; PRT; 188 AA.

AC P16762;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 01-JUN-1994 (Rel. 29, Last annotation update)

DE Hypothetical protein UL26.

GN UL26.

OS Human cytomegalovirus (strain AD169).

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Betaherpesvirinae; Cytomegalovirus.

OX NCBI_TaxID=10360;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE-90269039; PubMed-2161319;

RA Chee M.S., Bankier A.T., Beck S., Bohm R., Brown C.M., Cerny R.,

RA Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A.,

RA Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barré G.,

RA "Analysis of the protein-coding content of the sequence of human

cytomegalovirus strain AD169.";

RT cytomegalovirus strain AD169.";

RL Curr. Top. Microbiol. Immunol. 154:125-169(1990).

CC - SIMILARITY: BELONGS TO THE US22 FAMILY.

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CC EMBL; X17403; CA35425.1;

DR PIR; S09789; S09789.

KW Hypothetical protein.

FT CARBOHYD 136 136

SQ SEQUENCE 188 AA; 21155 MW; 57EA40349212FEB8 CRC64;

N-LINKED (GLCNAC...) (POTENTIAL).

Alignment Scores:

Pred. No.: 44.9 Length: 188

Score: 8.00 Matches: 8

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.16% Indels: 0

DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x UL26_HCMVA (1-188)

QY 1212 GTGTCGCGACGACGACGCTC 1189

Db 101 ValValArgAlaAlaAspSerLeu 108

RESULT 10

TNF7_HUMAN

ID TNF7_HUMAN STANDARD; PRT; 193 AA.

AC P32970; Q96J57;

DT 01-OCT-1993 (Rel. 27, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 7 (CD27 ligand) (CD27-

L) (CD70 antigen).

GN TNFSF7 OR CD70 OR CD27LG OR CD27L.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-B-cell;

RA MEDLINE-93258810; PubMed-8387892;

RA Goodwin R.G., Alderson M.R., Smith C.A., Armitage R.J., Vandenbos T.,

RA Jerzy R., Tough T.W., Schoenborn M.A., David-Smith T., Hennen K.,

RA Falk B., Cosman D., Baker E., Sutherland G.R., Grabstein K.H.,

RA Farrah T., Giri J.G., Beckmann M.P.;

RA "Molecular and biological characterization of a ligand for CD27

defines a new family of cytokines with homology to tumor necrosis

factor.";

RL Cell 73:447-456(1993).

RN [2]

RP SEQUENCE FROM N.A.

RA MEDLINE-94165470; PubMed-8120384;

RA Bowman M.R., Cullmins M.A., Yetz-Aldape J., Kriz R., Kelleher K.,

RA Herrmann S.;

RA "The cloning of CD70 and its identification as the ligand for CD27.";

RL J. Immunol. 152:1756-1761(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-Kidney;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cytokine that binds to TNFSF7/CD27. Plays a role in T
CC cell activation. Induces the proliferation of costimulated T cells
CC and enhances the generation of cytolytic T cells.
CC
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD70 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd70.htm".
CC
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DR EMBL; L08096; AAA36175.1; -
DR EMBL; S69339; AAB30121.1; -
DR EMBL; BC000725; AAH00725.1; -
DR PIR; A40738; A40738.
DR Genew; HGNC:11937; TNFSF7.
DR MIM; 602840; -
DR InterPro; IPR003637; TNF_7.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD036400; TNF_7; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
DR Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Antigen.
KW DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 21 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT FT (POTENTIAL).
FT FT EXTRACELLULAR (POTENTIAL).
FT FT POTENTIAL.. (GLNAC. . .) (POTENTIAL).
FT FT N-LINKED (GLNAC. . .) (POTENTIAL).
FT FT CARBOHYD 170 170 N-LINKED (GLNAC. . .) (POTENTIAL).
FT FT CONFLICT 154 154 A -> V (IN REF. 1).
SQ SEQUENCE 193 AA; 21118 MW; 9265856E33BEAD50 CRC64;

Alignment Scores:
Pred. No.: 44.7 Length: 193
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x TNF7_HUMAN (1-193)
QY 1734 CAGGGAGCCCGCGCTGGGACGC 1757
Db 76 GINGLYGLYPROALALEUGLYARG 83

RESULT 11
KTHY_HUMAN
ID KTHY_HUMAN
AC P23919; STANDARD; PRT; 212 AA.
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Thymidylate kinase (EC 2.7.4.9) (dTMP kinase).
GN DTYRK OR TYRK OR TWPK OR CDC8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91204436; PubMed=2017365;
RA Su J.Y., Sclafani R.A.;
RT "Molecular cloning and expression of the human deoxythymidylate kinase
RT gene in yeast.";
RL Nucleic Acids Res. 19:823-827(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94296549; PubMed=8024690;
RA Huang S.H., Tang A., Drisco B., Zhang S.Q., Seeger R., Li C.,
RA Jong A.;
RT "Human dTMP kinase: gene expression and enzymatic activity coinciding
RT with cell cycle progression and cell growth.";
RL DNA Cell Biol. 13:461-471(1994).
CC -1- FUNCTION: CATALYZES THE CONVERSION OF dTMP TO dTDP.
CC -1- CATALYTIC ACTIVITY: ATP + thymidine 5'-phosphate -> ADP + thymidine
CC 5'-diphosphate.
CC
CC -1- PATHWAY: SYNTHESIS OF dTTP FROM dTMP.
CC
CC -1- SIMILARITY: BELONGS TO THE THYMIDYLATE KINASE FAMILY.
CC
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DR EMBL; X54729; CAA38528.1; -
DR EMBL; L16991; AAA21719.1; -
DR PIR; S26845; S26845.
DR HSSP; P00572; ITMK.
DR Genew; HGNC:3061; DTYMK.
DR MIM; 188345; -
DR InterPro; IPR000062; Thymidylate_kin.
DR Pfam; PF02223; Thymidylate_kin; 1.
DR TIGRFAMs; TIGR000041; dTMP_kinase; 1.
DR PROSITE; PS01331; THYMIDYLATE_KINASE; 1.
KW Transferase; Kinase; Nucleotide biosynthesis; ATP-binding.
FT NP_BIND 13 20 ATP (PROBABLE).
FT CONFLICT 31 37 CAAGHEA -> SRGPPP (IN REF. 1).
FT CONFLICT 58 58 Q -> K (IN REF. 2).
FT CONFLICT 183 184 RL -> SI (IN REF. 2).
SQ SEQUENCE 212 AA; 23902 MW; E42876G25E61D3CB CRC64;

Alignment Scores:
Pred. No.: 44.1 Length: 212
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x KTHY_HUMAN (1-212)
QY 105 GCAGCAGGCCACAGGCAGCACTG 82
Db 32 AlaAlaGlyHisArgAlaGluLeu 39

RESULT 12
POL1_POPJA
ID POL1_POPJA STANDARD; PRT; 245 AA.
AC Q03276;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Retrovirus-related POL polypeptide from type I retrotransposable
DE element R1 [Contains: Reverse transcriptase (EC 2.7.7.49);
DE Endonuclease] (Fragment).
OS Popillia japonica (Japanese beetle).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

CC Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
 CC Scarabaeiformia; Scarabaeidae; Rutelinae; Popillia.
 CC NCBI_TaxID=7064;
 RN [1]
 RX MEDLINE=93196484; PubMed=8383793;
 RA Burke W.D., Eickbush D.G., Xiong Y., Jakubczak J.L., Eickbush T.H.;
 RA "Sequence relationship of retrotransposable elements RI and R2 within
 RT and between divergent insect species.";
 RL Mol. Biol. Evol. 10:163-185(1993).
 CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
 CC + [DNA] (N).
 CC -----
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 CC -----
 CC EMBL; L00944; AAA29783.1;
 DR PIR; F44490; F44490.
 DR Transferase; RNA-directed DNA polymerase; Transposable element;
 KW Hydrolase; Nuclease; Endonuclease.
 FT NON_TER 1
 FT DOMAIN <1 105 REVERSE TRANSCRIPTASE.
 FT DOMAIN 106 245 NUCLEIC ACID-BINDING ENDONUCLEASE.
 SQ SEQUENCE 245 AA; 28406 MW; 44D5C5C5E0D6166 CRC64;
 Alignment Scores:
 Pred. No.: 43.1 Length: 245
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.15% Indels: 0
 DB: 1 Gaps: 0
 US-09-824-647-16 (1-2095) x POLI_POPJA (1-245)
 QY 1494 CTGCGAGAGGAGGTCTCTGC 1517
 Db 168 LeuargGluGlySerGlyLeuGlyCys 175
 RESULT 13
 BCCP_SOYBN
 ID BCCP_SOYBN STANDARD; PRT; 262 AA.
 AC Q42783;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Biotin carboxyl carrier protein of acetyl-CoA carboxylase, chloroplast
 DE precursor (BCCP).
 GN ACCB-1.
 OS Glycine max (Soybean).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 CC NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=cv. Resnik;
 RA Reverdatto S.V., Bellinson V., Neilsen N.C.;
 RT "Characterization of a cDNA clone encoding a BCCP subunit of acetyl-
 RT CoA carboxylase from soybean."
 RL (In) Plant Gene Register PCR96-040.
 CC -!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A
 CC CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CATALYZES THE
 CC CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE
 CC TRANSFERS THE CARBOXYL GROUP TO FORM MALONYL-COA.
 CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first step.
 CC -!- SUBCELLULAR LOCATION: Chloroplast.
 CC -----

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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U40666; AAB67936.1;
 DR HSP; P02905; 3BD0.
 DR InterPro; IPR001249; AcCoA_biotinCC.
 DR InterPro; IPR001882; Biotin_attach.
 DR InterPro; IPR000089; Biotin_lipoyl.
 DR Pfam; PF00364; biotin_lipoyl; 1.
 DR PRINTS; PR01071; ACOABBIOTINCC.
 DR TIGRFAMs; TIGR00531; BCCP; 1.
 DR PROSITE; PS00188; BIOTIN; 1.
 KW Fatty acid biosynthesis; Biotin; Chloroplast; Transit peptide.
 FT TRANSIT 1 47 CHLOROPLAST.
 FT CHAIN 48 262 BIOTIN CARBOXYL CARRIER PROTEIN OF
 FT ACETYL-COA CARBOXYLASE.
 FT BINDING 227 227 BIOTIN (BY SIMILARITY).
 SQ SEQUENCE 262 AA; 27657 MW; 79B273BD8B87DF48 CRC64;
 Alignment Scores:
 Pred. No.: 42.6 Length: 262
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.16% Indels: 0
 DB: 1 Gaps: 0
 US-09-824-647-16 (1-2095) x BCCP_SOYBN (1-262)
 QY 1404 CCAGCTCCACCCCTGGCTCGGCA 1381
 Db 161 ProAlaProThrLeuAlaArgAla 168
 RESULT 14
 CIT2_MOUSE
 ID CIT2_MOUSE STANDARD; PRT; 269 AA.
 AC Q35740; Q35741; Q35742; Q35743; Q55198;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cbp/p300-interacting transactivator 2 (MSG-related protein 1) (MRG1
 DE protein).
 GN CITED2 OR MRG1 OR MSG2.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
 RC STRAIN=C57BL/6 X DBA;
 RX MEDLINE=98202510; PubMed=9533950;
 RA Dunwoody S.L., Rodriguez T.A., Beddington R.S.P.;
 RT "Mgsl and Mrgl, founding members of a gene family, show distinct
 RT patterns of gene expression during mouse embryogenesis.";
 RL Mech. Dev. 72:27-40(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RX MEDLINE=98094278; PubMed=9434189;
 RA Shioda T., Fenner M.H., Isselbacher K.J.;
 RT "Mgsl and its related protein MRG1 share a transcription activating
 RT domain.";
 RL Gene 204:235-241(1997).
 CC -!- FUNCTION: Interferes with the binding of transcription factors
 CC HIF-1a and STAT2 to p300/CBP (By similarity).
 CC -!- SUBUNIT: Binds to the p300/CBP CH1 region (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- ALTERNATIVE PRODUCTS: 4 isoforms; 1 (shown here), 2, 3 and 4; are
 CC produced by alternative splicing.

CC CC 1- SIMILARITY: BELONGS TO THE CITED FAMILY.

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CC EMBL; Y15163; CAA75432.1; -

CC EMBL; Y15163; CAA75433.1; -

CC EMBL; Y15163; CAA75434.1; -

CC EMBL; Y15163; CAA75435.1; -

CC EMBL; U86445; AAC39945.1; -

CC MGD; MGI:1306784; Cited2.

CC Transcription regulation; Nuclear protein; Alternative splicing.

CC KW DOMAIN 21 57 HIS-RICH.

CC FT DOMAIN 162 197 GLY-RICH.

CC FT DOMAIN 218 257 ASP/GLU-RICH (ACIDIC).

CC FT VARSPLIC 138 158 MISSING (IN ISOFORM 2).

CC FT VARSPLIC 159 213 MISSING (IN ISOFORM 3).

CC FT VARSPLIC 203 213 MISSING (IN ISOFORM 4).

CC SQ SEQUENCE 269 AA; 28382 MW; AFACDDSD57902A48 CRC64;

Alignment Scores:

Pred. No.:	42.5	Length:	269
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.16%	Indels:	0
DB:	1	Gaps:	0

US-09-824-647-16 (1-2095) x CIT2_MOUSE (1-269)

QY 1231 GCTGGGGGACGAGCTGCTGGT 1208

Db 186 AlAGlyGlySerAlAGlyGly 193

RESULT 15

CRK_XENLA

ID CRK_XENLA STANDARD; PRT; 296 AA.

AC P87378; 1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE SH2/SH3 adaptor crk (Adaptor molecule crk) (CRK2).

GN CRK.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae; Xenopodinae; Xenopus.

OC NCBI_TaxID=8355;

GN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-9718926; PubMed-9029144;

RA Evans E.K., Lu W., Strum S.L., Mayer B.J., Kornbluth S.;

RT "Crk is required for apoptosis in Xenopus egg extracts.";

RL EMBO J. 16:230-241(1997).

CC 1- FUNCTION: REQUIRED FOR APOPTOSIS IN XENOPUS EGG EXTRACTS.

CC 1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.

CC 1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.

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CC EMBL; U89774; BAB49698.1; -

CC HSSP; Q64010; ICKA.

DR InterPro; IPR000980; SH2.

DR InterPro; IPR001452; SH3.

DR Pfam; PF00017; SH2; 1.

DR Pfam; PF00018; SH3; 1.

DR PRINTS; PR00401; SH2DOMAIN.

DR PRINTS; PR00452; SH3DOMAIN.

DR PRODOM; PD000066; SH3; 1.

DR PRODOM; PD000093; SH2; 1.

DR SMART; SM00252; SH2; 1.

DR SMART; SM00326; SH3; 2.

DR PROSITE; PS50001; SH2; 1.

DR PROSITE; PS50002; SH3; 1.

KW SH2 domain; SH3 domain; Repeat.

FT DOMAIN 13 112 SH2.

FT DOMAIN 125 185 SH3 1.

FT DOMAIN 249 289 SH3 2.

SQ SEQUENCE 296 AA; 33409 MW; 544F11F4A1F75A66 CRC64;

Alignment Scores:

Pred. No.:	41.8	Length:	296
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.16%	Indels:	0
DB:	1	Gaps:	0

US-09-824-647-16 (1-2095) x CRK_XENLA (1-296)

QY 40 AGGCCACCAGCTCACCAGGCTCC 17

Db 184 ArgProSerSerProGlySer 191

RESULT 16

EFB1_CHICK

ID EFB1_CHICK STANDARD; PRT; 334 AA.

AC O73612; 1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Ephrin-B1 precursor (CEK5 ligand) (CELS-L).

GN EFNBL.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianinae; Gallus.

OC NCBI_TaxID=9031;

GN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-9723524; PubMed-9070326;

RA Holash J.A., Soans C., Chong L.D., Shao H., Dixit V.M., Pasquale E.B.;

RT "Reciprocal expression of the Eph receptor Cek5 and its ligand(s) in the early retina.";

RL Dev. Biol. 182:256-269(1997).

CC 1- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASE EPHB2.

CC 1- SUBCELLULAR LOCATION: Type I membrane protein.

CC 1- PTM: INDUCIBLE PHOSPHORYLATION OF TYROSINE RESIDUES IN THE CYTOPLASMIC DOMAIN (BY SIMILARITY).

CC 1- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.

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CC EMBL; U72394; AAC07986.1; -

CC InterPro; IPR001799; Ephrin.

CC Pfam; PF00812; Ephrin; 1.

CC PRINTS; PR01347; EPHRIN.

CC PRODOM; PD002533; Ephrin; 1.

DR PROSITE; PS01299; EPHRIN; 1.
KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 334 EPHRIN-B1.
FT DOMAIN 26 231 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 232 252 POTENTIAL.
FT DOMAIN 253 334 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 332 334 PDZ RECOGNITION MOTIF (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 334 AA; 36858 MW; 48AF556E9ED56CD5 CRC64;

Alignment Scores:
Pred. No.: 41.1 Length: 334
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x EFBI_CHICK (1-334)
QY 438 GTGCGATGGCTCTGGGGTGTG 461
Db 7 GlyArgTrpLeuGlyValLeu 14

RESULT 17
K6PF_SYNY3
ID K6PF_SYNY3 STANDARD; PRT; 361 AA.
AC P72830;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)
DE (Phosphofructokinase).
GN PFKA OR SL1196.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirose M., Sugita M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
CC fructose 1,6-bisphosphate.
CC -1- PATHWAY: KEY CONTROL STEP OF GLYCOLYSIS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOFRUCTOKINASE FAMILY.

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EMBL; D90901; BAA16845.1;
DR HSP98; P06998; 2PFK.
DR InterPro; IPR000023; Ppf fructokinase.
DR Pfam; PF00365; PFK; 1.
DR PRINTS; PR00476; PPFRTKINASE.
DR ProDom; PD000707; Ppf fructokinase; 1.
DR PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 1.
KW Kinase; transferase; Glycolysis; Complete proteome.

SQ SEQUENCE 361 AA; 38588 MW; 96A83E05F318552C CRC64;

Alignment Scores:
Pred. No.: 40.6 Length: 361
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x K6PF_SYNY3 (1-361)
QY 1152 TTGCGACGAGTATCGGAGGAGG 1129
Db 193 LeuAlaAlaGlyGlyGly 200

RESULT 18
NPT4_HUMAN
ID NPT4_HUMAN STANDARD; PRT; 401 AA.
AC O00476;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium-dependent phosphate transport protein 4 (Sodium/phosphate
DE cotransporter 4) (Na(+)/PI cotransporter 4).
GN SLC17A4 OR NPT4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97294057; PubMed=9149941;
RA Ruddy D.A., Kronmal G.S., Lee V.K., Mintier G.A., Quintana L.,
RA Domingo R. Jr., Meyer N.C., Irrinki A., McClelland E.E., Fullan A.,
RA Mapa F.A., Moore T., Thomas W., Loeb D.B., Harmon C., Tsuchihashi Z.,
RA Wolff R.K., Schatzman R.C., Feder J.N.;
RT "A 1.1-Mb transcript map of the hereditary hemochromatosis locus.";
RL Genome Res. 7:441-456(1997).
CC -1- FUNCTION: MAY BE INVOLVED IN ACTIVELY TRANSPORTING PHOSPHATE
CC INTO CELLS VIA NA+ COTRANSPORT (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

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EMBL; U90545; AAB53423.1;
DR Genew; HGNC:10931; SLC17A3.
DR MIM; 604216;
DR Transport; Symport; Sodium transport; Transmembrane; Glycoprotein;
KW Phosphorylation.
FT TRANSMEM 20 40 POTENTIAL.
FT TRANSMEM 108 128 POTENTIAL.
FT TRANSMEM 135 155 POTENTIAL.
FT TRANSMEM 200 220 POTENTIAL.
FT TRANSMEM 237 257 POTENTIAL.
FT TRANSMEM 285 305 POTENTIAL.
FT TRANSMEM 338 358 POTENTIAL.
FT TRANSMEM 366 386 POTENTIAL.
FT CARBOHYD 41 41 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 49 49 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 58 58 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 401 AA; 44051 MW; 52359B2091948285 CRC64;

Alignment Scores:
Pred. No.: 39.9 Length: 401
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x NP74_HUMAN (1-401)

QY 380 CCATCCAGTCCCTGATGATGTCAGT 403
Db 281 ProserSerAlaLeuIleValSer 288

RESULT 19

AA74_ARATH STANDARD; PRT; 403 AA.

AC P46646; Q9S169;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Aspartate aminotransferase, cytoplasmic isozyme 2 (EC 2.6.1.1)
DE (Transaminase A).
GN ASP4 OR ATL62800 OR F23N19.17 OR F23N19.26.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia; TISSUE=Leaf;
RX MEDLINE=95201829; PubMed=7894512;
RA Schultz C.J., Coruzzi G.M.;
RT "The aspartate aminotransferase gene family of Arabidopsis encodes
RT isoenzymes localized to three distinct subcellular compartments.";
RL Plant J. 7:61-75(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altai H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway T.H., Dewar K.,
RA Dunn P., Egu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gull J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.B., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Laugin-Hopfer S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pail G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:816-820(2000).
CC -1- FUNCTION: IMPORTANT FOR THE METABOLISM OF AMINO ACIDS AND KREBS-
CC CYCLE RELATED ORGANIC ACIDS. IN PLANTS, IT IS INVOLVED IN NITROGEN
CC METABOLISM AND IN ASPECTS OF CARBON AND ENERGY METABOLISM.
CC -1- CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate -> oxaloacetate +
CC L-glutamate.
CC -1- COPACITOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (potential).
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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CC or send an email to license@isb-sib.ch)
CC -----
CC DR EMBL; U15035; AAA79372.1;
CC DR EMBL; AC007190; AAF19543.1; ALT_SEQ.
CC DR HSP; P00508; 7AAT.
CC DR InterPro; IPR004839; Aminotransf1/2.
CC DR InterPro; IPR000796; Aspttransf_sub.
CC DR InterPro; IPR004838; NHtransf_1.
CC DR Pfam; PF00155; aminotran_1_2; 1.
CC DR PRINTS; PR00799; TRANSAMINASE.
CC DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
CC KW Transferase; Aminotransferase; Pyridoxal phosphate; Multigene family.
FT BINDING 249 249 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT CONFLICT 199 199 I -> F (IN REF. 1).
SQ SEQUENCE 403 AA; 44358 MW; 6C6046EF6F970216 CRC64;

Alignment Scores:

Pred. No.:	39.9	Length:	403
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.16%	Indels:	0
DB:	1	Gaps:	0

US-09-824-647-16 (1-2095) x AAT4_ARATH (1-403)

QY 465 GGGGAGCAGCCCCAGGAGGCATC 442
Db 169 GlyAlaAlaProGlyAlaIle 176

RESULT 20

RA_FUGRU STANDARD; PRT; 447 AA.

AC Q9W523; Q9W524;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Retinoic acid receptor alpha (RAR-alpha).
GN RARA OR NR1B1.
OS Fuqu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99384012; PubMed=10452951;
RA Wentworth J.M., Schoenfeld V., Meek S., Elgar G., Brenner S.,
RA Chatterjee K.K.;
RT "Isolation and characterization of the retinoic acid receptor-alpha
RT gene in the Japanese pufferfish, F. rubripes.";
RL Gene 236:315-323(1999).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR RETINOIC ACID. THIS METABOLITE
CC HAS PROFOUND EFFECTS ON VERTEBRATE DEVELOPMENT. RETINOIC ACID IS
CC A MORPHOGEN AND IS A POWERFUL TERATOGEN. THIS RECEPTOR CONTROLS
CC CELLS FUNCTIONS BY DIRECTLY REGULATING GENE EXPRESSION.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-1 (SHOWN HERE) AND ALPHA-
CC 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
CC NRI SUBFAMILY.
CC -----
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```
CC CC EMBL; AJ012382; CAB96754.1;
CC DR EMBL; AJ012380; CAB96754.1; JOINED.
CC DR EMBL; AJ012381; CAB93979.1;
CC DR EMBL; AJ012380; CAB93979.1; JOINED.
CC DR EMBL; AJ012378; CAB93870.1;
CC DR EMBL; AJ012379; CAB93871.1;
CC DR HSSP; P10826; IHRA.
CC DR InterPro; IPR000536; Hormone_rec_lig.
CC DR InterPro; IPR01628; znf_C4steroid.
CC DR Pfam; PF00104; hormone_rec; 2.
CC DR Pfam; PF00105; zf-C4; 2.
CC DR PRINTS; PR00047; STROIDFINGER.
CC DR ProDom; PD000035; znf_C4steroid; 1.
CC DR SMART; SM00430; HOL1; 1.
CC DR SMART; SM00399; znf_C4; 1.
CC DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
CC Zinc-finger; Multigene family; Alternative splicing.
CC KW DOMAIN 1 79
CC FT DNA_BIND 80 145
CC FT ZN_FING 80 100
CC FT ZN_FING 116 140
CC FT ZN_FING 146 191
CC FT DOMAIN 192 411
CC FT VARSPLIC 1 52
CC FT
CC FT
CC FT
CC FT
CC FT
CC SQ SEQUENCE 447 AA; 49532 MW; E00630F720B1508D CRC64;

Alignment Scores:
Pred. No.: 39,3 Length: 447
Score: 8,00 Matches: 8
Percent Similarity: 100,00% Conservativeness: 0
Best Local Similarity: 100,00% Mismatches: 0
Query Match: 1,16% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x RRA_FUGRU (1-447)
QY 1423 GGGGCACTGGCAGCAGGCCGACG 1400
DB 415 GlyAlaThrGlySerArgProSer 422

RESULT 21
VSG7_TRYBR
ID VSG7_TRYBR STANDARD; PRT; 467 AA.
AC P02898;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Variant surface glycoprotein 7 (VSG 7) (Metacyclic variable antigen)
DE (fragments).
OS Trypanosoma brucei rhodesiense.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=31286;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85038570; PubMed=6593722;
RA Lenardo M.J., Rice-Ficht A.C., Kelly G., Esser K.M., Donelson J.B.;
RT "Characterization of the genes specifying two metacyclic variable
RT antigen types in Trypanosoma brucei rhodesiense."
RL Proc Natl Acad Sci U S A. 81:6642-6646(1984).
CC -1- FUNCTION: VSG FORMS A COAT ON THE SURFACE OF THE PARASITE. THE
CC TYRANOSOME EVADES THE IMMUNE RESPONSE OF THE HOST BY EXPRESSING
CC A SERIES OF ANTIGENICALLY DISTINCT VSGS FROM AN ESTIMATED 1000
CC VSG GENES.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC A SOLUBLE FORM IS RELEASED FROM RUPTURED CELLS BY THE ACTION OF A
CC PI-PLC.
CC PIR; A03393; VMT07R.
```

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KW Glycoprotein; Antigen; Trypanosomiasis; GPI-anchor; Membrane.
FT NON_TER 1 88
FT NON_CONS 87 444
FT CHAIN <1 444
FT PROPEP 445 467
FT CARBOHYD 108 252
FT CARBOHYD 252 416
FT CARBOHYD 416 444
FT LIPID 444 444
FT GPI-ANCHOR.
SQ SEQUENCE 467 AA; 49963 MW; 3A4805AFFBECA686 CRC64;

Alignment Scores:
Pred. No.: 39 Length: 467
Score: 8,00 Matches: 8
Percent Similarity: 100,00% Conservativeness: 0
Best Local Similarity: 100,00% Mismatches: 0
Query Match: 1,16% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x VSG7_TRYBR (1-467)
QY 1632 GCCCTGCGGTGTCTCGGCAGCA 1609
DB 454 AlaLeuSerValSerAlaAla 461

RESULT 22
DGT1_HUMAN
ID DGT1_HUMAN STANDARD; PRT; 488 AA.
AC Q75907;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Diacylglycerol O-acyltransferase 1 (EC 2.3.1.20) (Diglyceride
DE acyltransferase) (ACAT related gene product 1).
GN DGAT1 OR DGAT OR AGRP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98434592; PubMed=9756920;
RA Oelkers P., Behari A., Cromley D., Billheimer J.T., Sturley S.L.;
RT "Characterization of two human genes encoding acyl coenzyme
RT A:cholesterol acyltransferase-related enzymes."
RL J. Biol. Chem. 273:26765-26771(1998).
CC -1- FUNCTION: Catalyzes the terminal and only committed step in
CC triacylglycerol synthesis by using diacylglycerol and fatty acyl
CC CoA as substrates.
CC -1- CATALYTIC ACTIVITY: Acyl-CoA + 1,2-diacylglycerol -> CoA +
CC triacylglycerol.
CC -1- PATHWAY: Central role in the metabolism of cellular diacylglycerol
CC lipids.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (By similarity).
CC -1- SIMILARITY: BELONGS TO THE STEROL O-ACYLTRANSFERASE FAMILY.
CC
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FT TRANSMEM 166 186 POTENTIAL.
 FT TRANSMEM 189 209 POTENTIAL.
 FT TRANSMEM 282 302 POTENTIAL.
 FT TRANSMEM 332 352 POTENTIAL.
 FT TRANSMEM 406 426 POTENTIAL.
 FT TRANSMEM 428 448 POTENTIAL.
 FT TRANSMEM 453 473 POTENTIAL.
 SQ SEQUENCE 488 AA; 55252 MW; 12E34BA/478ABALF CRC64;

Alignment Scores:
 Pred. No.: 38.7 Length: 488
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.16% Indels: 0
 DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x DGT1_HUMAN (1-488)

OY 1417 ACTGGCAGCAGCCGAGCTCCAC 1394
 DB 12 ThrGlySerArgProSerSerHis 19

RESULT 23

DGT1_CERAE
 ID DGT1_CERAE STANDARD; PRT; 491 AA.

AC Q9GME1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Diacylglycerol O-acyltransferase 1 (EC 2.3.1.20) (Diglyceride acyltransferase).
 GN DGAT1 OR DGAT.

OS Cercopithecus aethiops (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.

NCBI_TaxID=9534;

[1]

SEQUENCE FROM N.A.

RA Joyce C.W., Davis M.A., Anderson R.A., Rudel L.L.;

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Catalyzes the terminal and only committed step in triacylglycerol synthesis by using diacylglycerol and fatty acyl CoA as substrates.

CC -1- CATALYTIC ACTIVITY: Acyl-CoA + 1,2-diacylglycerol = CoA + triacylglycerol.

CC -1- PATHWAY: Central role in the metabolism of cellular diacylglycerol lipids.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum (By similarity).

CC -1- SIMILARITY: BELONGS TO THE STEROL O-ACYLTRANSFERASE FAMILY.

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CC EMBL; AF236018; AAF98557.1;
 DR InterPro; IPR002688; ACAT.
 DR Pfam; PF01800; ACAT; 1.

KW Transferase; Acyltransferase; Transmembrane; Endoplasmic reticulum.

FT TRANSMEM 107 127 POTENTIAL.
 FT TRANSMEM 131 151 POTENTIAL.
 FT TRANSMEM 169 189 POTENTIAL.
 FT TRANSMEM 192 212 POTENTIAL.
 FT TRANSMEM 285 305 POTENTIAL.
 FT TRANSMEM 335 355 POTENTIAL.
 FT TRANSMEM 404 424 POTENTIAL.

FT TRANSMEM 431 451 POTENTIAL.
 FT TRANSMEM 456 476 POTENTIAL.
 SQ SEQUENCE 491 AA; 55643 MW; BFD3683453D588DB CRC64;

Alignment Scores:
 Pred. No.: 38.7 Length: 491
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.16% Indels: 0
 DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x DGT1_CERAE (1-491)

OY 1417 ACTGGCAGCAGCCGAGCTCCAC 1394
 DB 15 ThrGlySerArgProSerSerHis 22

RESULT 24

UAP1_ARATH
 ID UAP1_ARATH STANDARD; PRT; 502 AA.

AC O64765;
 DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Probable UDP-N-acetylglucosamine pyrophosphorylase (EC 2.7.7.23).
 GN AT2G35020 OR F1913.25.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.

NCBI_TaxID=3702;

[1]

SEQUENCE FROM N.A.

RP SPRAIN-cv. Columbia;

RX MEDLINE=2008348; PubMed=10617197;

RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,

RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,

RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,

RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,

RA Niernman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,

RA Venter J.C.;

RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis

RL thaliana."

RL Nature 402:761-768(1999).

CC -1- CATALYTIC ACTIVITY: UTP + N-acetyl-alpha-D-glucosamine 1-phosphate

CC - diphosphate + UDP-N-acetyl-D-glucosamine.

CC -1- PATHWAY: UDP-GlcNAc biosynthesis from Fru-6-P; fourth (last

CC step.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

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CC EMBL; AC004238; AAC12841.1;

DR InterPro; IPR002618; UDPGP.

DR Pfam; PF01704; UDPGP; 1.

KW Transferase; Nucleotidyltransferase.

FT SITE 133 133 BINDING SITE FOR HEXNAC-1-P (BY SIMILARITY).

FT ACT_SITE 137 137 POTENTIAL.

FT ACT_SITE 144 144 POTENTIAL.

SQ SEQUENCE 502 AA; 55759 MW; 72C0F2DCF15ACAD7 CRC64;

Alignment Scores:

Pred. No.: 38.5 Length: 502

Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: Gaps: 0

US-09-824-647-16 (1-2095) x UNPLARATH (1-502)
QY 242 TCTCAGGAGCTTCACGTCTGCTGCC 265
Db 82 SerGlnGlyLeuProValAlaAla 89

RESULT 25
VSAL_TRYBB STANDARD; PRT; 503 AA.
ID VSAL_TRYBB STANDARD; PRT; 503 AA.
AC P06015: Q26722;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Variant surface glycoprotein Antat 1.1 precursor (VSG) (Expression-linked copy) (ELC).
OS Trypanosoma brucei.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID:5702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-84028590; PubMed-6313354;
RA Michiels F., Matthysens G., Kronenberger P., Pays E., Dero B.,
RA van Assel S., Darrille M., Cravador A., Steinert M., Hamers R.,
RT "Gene activation and re-expression of a Trypanosoma brucei variant surface glycoprotein."
RT surface glycoprotein."
RL EMBO J. 2:1185-1192(1983).
RN [2]
RP SEQUENCE OF 1-416 FROM N.A.
RC STRAIN-EATRO 1125;
RX MEDLINE-90214610; PubMed-2323332;
RA van der Werf A., van Assel S., Aerts D., Steinert M., Pays E.,
RT "Telomere interactions may condition the programming of antigen expression in Trypanosoma brucei."
RL EMBO J. 9:1035-1040(1990).
RN [3]
RP SEQUENCE OF 391-503 FROM N.A.
RX MEDLINE-82013622; PubMed-7278981;
RA Matthysens G., Michiels F., Hamers R., Pays E., Steinert M.;
RT "Two variant surface glycoproteins of Trypanosoma brucei have a conserved C-terminus."
RL Nature 293:230-233(1981).
RN [4]
RP SEQUENCE OF 270-344 FROM N.A.
RX MEDLINE-86028178; PubMed-4053185;
RA Pays E., Houard S., Pays A., van Assel S., Dupont F., Aerts D.,
RA Huet-Duvillier G., Gomes V., Richet C., Degand P., van Meirvenne N.,
RA Steinert M.;
RT "Trypanosoma brucei: The extent of conversion in antigen genes may be related to the DNA coding specificity."
RL Cell 42:821-829(1985).
CC -1- FUNCTION: VSG FORMS A COAT ON THE SURFACE OF THE PARASITE. THE TYPANOSOME EVADES THE IMMUNE RESPONSE OF THE HOST BY EXPRESSING A SERIES OF ANTIGENICALLY DISTINCT VSGS FROM AN ESTIMATED 1000 VSG GENES.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. A SOLUBLE FORM IS RELEASED FROM RUPTURED CELLS BY THE ACTION OF A PI-PLC.
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CC EMBL; X01843; CAA25971.1;
DR

DR EMBL; X15817; CAA33809.1;
DR EMBL; M12005; AAA30162.1;
DR EMBL; J01213; AAA30280.1;
DR PIR; S07174; VMUT1B.
DR InterPro: IPR001812; Trypan_glycop.
DR Pfam; PF00913; Antigen; Trypanosomiasis; GPI-anchor; Membrane; Signal.
KW Glycoprotein; Antigen; Trypanosomiasis; GPI-anchor; Membrane; Signal.
FT SIGNAL 1 29
FT CHAIN 30 480
FT PROPEP 481 503
FT DISULFID 45 172
FT CARBOHYD 154 209
FT CARBOHYD 113 113
FT CARBOHYD 419 419
FT CARBOHYD 432 432
FT LIPID 480 480
FT CONFLICT 334 334
FT CONFLICT 346 346
FT CONFLICT 419 419
SQ SEQUENCE 503 AA; 52814 MW; 38541B93F6DF46C6 CRC64;
Alignment Scores: 38.5 Length: 503
Pred. NO.: 8.00 Matches: 8
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 1.15% Gaps: 0
DB: 1

US-09-824-647-16 (1-2095) x VSAL_TRYBB (1-503)
QY 1632 GCCCTGCTGCTGCTGCTGCGACGA 1609
Db 490 AlaLeuSerValValSerAlaAla 497

RESULT 26
VSIG6_TRYBB STANDARD; PRT; 503 AA.
ID VSIG6_TRYBB STANDARD; PRT; 503 AA.
AC P06014;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last annotation update)
DE Variant surface glycoprotein ILTAR 1.3 precursor (VSG).
OS Trypanosoma brucei.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID:5702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rice-Ficht A.C., Chen K.K., Donelson J.E.;
RT "Sequence homologues near the C-termini of the variable surface glycoproteins of Trypanosoma brucei."
RL Nature 294:53-57(1981).
CC -1- FUNCTION: VSG FORMS A COAT ON THE SURFACE OF THE PARASITE. THE TYPANOSOME EVADES THE IMMUNE RESPONSE OF THE HOST BY EXPRESSING A SERIES OF ANTIGENICALLY DISTINCT VSGS FROM AN ESTIMATED 1000 VSG GENES.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. A SOLUBLE FORM IS RELEASED FROM RUPTURED CELLS BY THE ACTION OF A PI-PLC.
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CC EMBL; J01221; AAA30288.1;
DR PIR; S09640; S09640.
DR InterPro: IPR001812; Trypan_glycop.
DR Pfam; PF00913; Trypan_glycop; 1.
KW Glycoprotein; Antigen; Trypanosomiasis; Signal; GPI-anchor; Membrane.

```
FT SIGNAL 1 29
FT CHAIN 30 480
FT PROPEP 481 503
FT DISULFID 42 168
FT DISULFID 150 206
FT CARBOHYD 419 419
FT CARBOHYD 432 432
FT LIPID 480 480
SQ SEQUENCE 503 AA; 54618 MW; 70144DB0408AA9A CRC64;

Alignment Scores:
Pred. No.: 38.5 Length: 503
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x VS16_TRYBB (1-503)
QY 1632 GCCCTGCTGGTGTCTCGCAGCA 1609
DB 490 AlaLeuSerValSerAlaAla 497

RESULT 27
YCP7_BRAJA
ID YCP7_BRAJA STANDARD; PRT; 516 AA.
AC 045221;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 55.4 kDa protein in CYP117 3'region (ORF7).
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RA Tully R.E., Keister D.L.;
FT "Cloning and mutagenesis of a cytochrome P-450 locus from
RT Bradyrhizobium japonicum that is expressed anaerobically and
RT symbiotically."
RL Appl. Environ. Microbiol. 59:4136-4142(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=98322110; PubMed=9655913;
RA Tully R.E., van Berkum P., Lovins K.W., Keister D.L.;
RT "Identification and sequencing of a cytochrome P450 gene cluster from
RT Bradyrhizobium japonicum."
RL Biochim. Biophys. Acta 1398:243-255(1998).
CC -1- SIMILARITY: CONTAINS 2 PFTB REPEATS.
CC
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CC
CC DR EMBL; U12678; AAC28895.1;
KW Hypothetical protein; Repeat. PFTB 1.
FT REPEAT 45 86
FT REPEAT 401 443 PFTB 2.
SQ SEQUENCE 516 AA; 55381 MW; 8C0660A0C7AFBCE5 CRC64;

Alignment Scores:
Pred. No.: 38.4 Length: 516
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 1 Gaps: 0
```

```
Query Match: 1.16% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x YCP7_BRAJA (1-516)
QY 2056 CAACACCCCTGTGGATAGGAA 2033
DB 473 GluThrProLeuTripleGlyLys 480

RESULT 28
VS13_TRYBB
ID VS13_TRYBB STANDARD; PRT; 532 AA.
AC P26328;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Variant surface glycoprotein ILTAT 1.23 precursor (VSG).
OS Trypanosoma brucei brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate M1AG 206;
RX MEDLINE=92046037; PubMed=1942032;
RA Carrington M., Miller N., Blum M.L., Roditi I., Wiley D.C.,
RA Turner M.J.;
RT "Variant specific glycoprotein of Trypanosoma brucei consists of two
RT domains each having an independently conserved pattern of cysteine
RT residues."
RL J. Mol. Biol. 221:823-835(1991).
CC -1- FUNCTION: VSG FORMS A COAT ON THE SURFACE OF THE PARASITE. THE
CC TYRANOSOME EVADES THE IMMUNE RESPONSE OF THE HOST BY EXPRESSING
CC A SERIES OF ANTIGENICALLY DISTINCT VSGS FROM AN ESTIMATED 1000.
CC VSG GENES.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC A SOLUBLE FORM IS RELEASED FROM RUPTURED CELLS BY THE ACTION OF A
CC PI-PLC.
CC
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CC
CC DR EMBL; X56768; CA440087.1;
DR PIR; S18448; S18448.
KW Glycoprotein; Antigen; Trypanosomiasis; GPI-anchor; Membrane; Signal.
FT SIGNAL 1 23
FT CHAIN 24 511
FT PROPEP 512 532
FT CARBOHYD 66 66
FT CARBOHYD 419 419
FT CARBOHYD 509 509
FT LIPID 511 511
SQ SEQUENCE 532 AA; 56778 MW; EED0D72C919396E6 CRC64;

Alignment Scores:
Pred. No.: 38.2 Length: 532
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x VS13_TRYBB (1-532)
QY 1632 GCCCTGCTGGTGTCTCGCAGCA 1609
DB 519 AlaLeuSerValSerAlaAla 526

RESULT 29
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EST3_RAT
ID EST3_RAT STANDARD; PRT; 561 AA.
AC Q63108;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Liver carboxylesterase 3 precursor (EC 3.1.1.1) (Carboxylesterase ES-3)
DE (PI 5.5 esterase) (ES-HREL).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=95032008; PubMed=7945287;
RA Robb M., Beaufay H.;
RT "Cloning and sequencing of rat liver carboxylesterase ES-3 (egasyn).";
RL Biochem. Biophys. Res. Commun. 203:1404-1411(1994).
CC -1- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN
CC THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O -> an alcohol + a
CC carboxylic anion.
CC -1- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic
CC reticulum.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC
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CC
CC EMBL; X81395; CAA57158.1; -
CC HSP; P21836; 1MAH.
CC InterPro: IPR002018; CarboxylesteraseB.
CC Pfam; PF00135; Coesterase; 1.
CC PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
CC PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
CC Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
KW Signal; Multigene family.
FT CHAIN 1 18 BY SIMILARITY.
FT ACT_SITE 19 561 LIVER CARBOXYLESTERASE 3.
FT ACT_SITE 221 221 BY SIMILARITY.
FT ACT_SITE 466 466 BY SIMILARITY.
FT DISULFID 87 116 BY SIMILARITY.
FT DISULFID 273 284 BY SIMILARITY.
FT SITE 558 561 PREVENT SECRETION FROM ER (POTENTIAL).
FT CARBOHYD 79 79 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 107 107 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 489 489 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 561 AA; 61714 MW; 1E14D66DF089B86F CRC64;

Alignment Scores:
Pred. No.: 37.9 Length: 561
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x EST3_RAT (1-561)
QY 34 GTGGCCTTACACAGCGGTGGTG 57
Db 249 VAlAlaLeuThrAlaGlyLeuVal 256
RESULT 30
ES22_MOUSE STANDARD; PRT; 562 AA.
ID ES22_MOUSE
```

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Q64176;
AC 01-NOV-1997 (Rel. 35, Created)
AC 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Liver carboxylesterase 22 precursor (EC 3.1.1.1) (Egasyn) (Esterase-
DE 22) (ES-22).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=92147141; PubMed=1783403;
RA Ovnik M., Svank R.T., Fletcher C., Zhen L., Novak E.K., Baumann H.,
RA Reintz N., Ganschow R.E.;
RT "Characterization and functional expression of a cDNA encoding egasyn
RT (esterase-22): the endoplasmic reticulum-targeting protein of beta-
RT glucuronidase."
RL Genomics 11:956-967(1991).
CC -1- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN
CC THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O -> an alcohol + a
CC carboxylic anion.
CC -1- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic
CC reticulum.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC
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CC
CC EMBL; S80191; AAB21335.1; -
CC HSP; P21836; 1MAH.
CC InterPro: IPR002018; CarboxylesteraseB.
CC InterPro; IPR000379; Ser_estrfs_site.
CC Pfam; PF00135; Coesterase; 1.
CC PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
CC PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
CC Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
KW Signal; Multigene family.
FT CHAIN 1 19 BY SIMILARITY.
FT ACT_SITE 20 562 LIVER CARBOXYLESTERASE 22.
FT ACT_SITE 222 222 BY SIMILARITY.
FT ACT_SITE 467 467 BY SIMILARITY.
FT DISULFID 88 117 BY SIMILARITY.
FT DISULFID 274 285 BY SIMILARITY.
FT SITE 559 562 PREVENT SECRETION FROM ER (POTENTIAL).
FT CARBOHYD 80 80 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 490 490 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 562 AA; 61581 MW; FB1A4367A0C8B2E3 CRC64;

Alignment Scores:
Pred. No.: 37.9 Length: 562
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x ES22_MOUSE (1-562)
QY 34 GTGGCCTTACACAGCGGTGGTG 57
Db 250 VAlAlaLeuThrAlaGlyLeuVal 257
RESULT 31
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DR	EMBL; U03864; AAB60351.1; -;
DR	EMBL; L31772; AAB59487.1; -;
DR	EMBL; S70782; AAB31163.2; -;
DR	EMBL; D29952; BAA06222.1; -;
DR	PIR; JH0447; JH0447.
DR	Genew; HGNC:280; ADRAID.
DR	MIM; 104219; -;
DR	InterPro; IPR000276; GPCR_Rhodpsn.
DR	Pfam; PF00001; 7tm_1; 1.
DR	PRINTS; PR00237; GPCRRHODPSN.
DR	PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR	PROSITE; PS00362; G_PROTEIN_RECP_F1_2; 1.
DR	G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein; Palmitate.
KW	MultiGene family; Phosphorylation; Phosphorylation; EXTRACELLULAR (POTENTIAL).
KW	DOMAIN 1 95
FT	TRANSMEM 96 131
FT	DOMAIN 122 133
FT	TRANSMEM 134 159
FT	DOMAIN 160 169
FT	TRANSMEM 170 192
FT	DOMAIN 193 213
FT	TRANSMEM 214 238
FT	DOMAIN 239 251
FT	TRANSMEM 252 275
FT	DOMAIN 276 348
FT	TRANSMEM 349 373
FT	DOMAIN 374 380
FT	TRANSMEM 381 405
FT	DOMAIN 406 572
FT	LIPID 419 419
FT	DOMAIN 422 428
FT	CONFLICT 1 83
FT	CONFLICT 31 31
FT	CONFLICT 489 572
FT	CONFLICT 522 522
FT	SEQUENCE 572 AA; 60462 MW; EBEB134CF20A4988 CRC64;
SQ	
Alignment Scores:	
Pred. No.:	37.8 Length: 572
Score:	8.00 Matches: 8
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	1.16% Indels: 0
DB:	1 Gaps: 0
US-09-824-647-16 (1-2095) x ALAD_HUMAN (1-572)	
QY	1231 GCTGGGCGCAGCTGCTGGTGGT 1208
DB	
DB	20 AlaglyglySerAlaglygly 27
RESULT 32	
YS50_MYCTU	
ID	YS50_MYCTU STANDARD; PRT; 629 AA.
AC	O05809;
DT	30-MAY-2000 (Rel. 39, Created)
DT	30-MAY-2000 (Rel. 39, Last sequence update)
DE	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Hypothetical protein RV2850c.
GN	RV2850C OR MT2916 OR MYCY24A.07.
OC	Mycobacterium tuberculosis.
OC	Bacteria; Actinobacteria; Actinobacteria (Class); Actinobacteridae;
OC	Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=H37Rv;


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RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE-Testis;
RX  MEDLINE-95394378; PubMed-7665101;
RA  Kida S., Umehara T., Horikoshi M.;
RT  "Three distinct regions in a rat TFIIID subunit containing histone H4
RL  homology.";
CC  GENE 161:303-304(1995).
CC  -1- FUNCTION: TFIIID IS A MULTIMERIC PROTEIN COMPLEX THAT PLAYS A
CC  CENTRAL ROLE IN MEDIATING PROMOTER RESPONSES TO VARIOUS ACTIVATORS
CC  AND REPRESSORS. BINDS TIGHTLY TO TAFII-250 AND ALSO DIRECTLY
CC  INTERACTS WITH TAFII-40.
CC  -1- SUBUNIT: TFIIID IS COMPOSED OF TATA BINDING PROTEIN (TBP) AND A
CC  NUMBER OF TBP-ASSOCIATED FACTORS (TAFs).
CC  -1- SUBCELLULAR LOCATION: Nuclear.
CC  -1- SIMILARITY: BELONGS TO THE TAF2E FAMILY.
CC  -----
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CC  -----
DR  EMBL; D49446; BAA08435.1; -
DR  InterPro; IPR004822; Histone_core.
DR  InterPro; IPR004823; TFIIID_TAF.
DR  Pfam; PF02969; TAF; 1.
KW  Transcription regulation; Nuclear protein.
SQ  SEQUENCE 678 AA; 72713 MW; 92D7225E3B7CC171 CRC64;

Alignment Scores:
Pred. No.: 36.8 Length: 678
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x T2D5_RAT (1-678)
QY 1053 GGCCCGACGTCACCTGAGCTGCG 1076
Db 670 GlyProSerProGlnProAla 677
|||||
RESULT 35
ROXN_HUMAN
ID ROXN_HUMAN STANDARD; PRT; 993 AA.
AC Q9UGR2; Q9UGP9; Q9UGQ9; Q9UGR0; Q9UGR1; Q9UGK3; Q9H8B6;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rotavirus 'X' associated non-structural protein (RoxAN).
GN KRAA1031.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20057165; PubMed-10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,
RA Clamp M., Smith L.J., Alnough R., Almeida J.P., Babbage A.K.,
RA Bagguely C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burdill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley N.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby V.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Graham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,

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RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann O.T.,
RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spraggon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chissole S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Benis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
RA Schest P., Walker C., Wansley A., Wohlmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L., Wardis E., Waterston R., Wilson R.,
RA Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L.,
RA McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelman L.,
RA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyraud M., Kedra D.,
RA Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
RA Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
RA Tikhunov Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495(1999).
[2]
RP SEQUENCE OF 1-780 FROM N.A. (ISOFORM 2).
RA Lindenbaum P.;
RT "RoxAN: a tetratricopeptide cellular protein interacting with
RT rotavirus non-structural protein NSP3.";
RL Thesis (2000), University of Paris XI, France.
[3]
RP SEQUENCE OF 1-208 FROM N.A.
RC TISSUE-Placenta;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
RA Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
RA Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE OF 38-993 FROM N.A. (ISOFORM 2).
RC TISSUE-Brain;
RX MEDLINE-99397452; PubMed-10470851;
RA Kikuno R., Nagase T., Ishikawa K.-I., Hirose M., Miyajima N.,
RA Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIV.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:197-205(1999).
CC -1- SUBUNIT: Interacts with the rotavirus non-structural protein
CC NSP3
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be
CC produced by alternative splicing.
CC -1- SIMILARITY: CONTAINS 1 TPR REPEATS.
CC -1- SIMILARITY: CONTAINS 2 C2H2-TYPE ZINC FINGERS.
CC -1- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
CC -----
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CC EMBL; AL035659; CAB62493.1; -
DR EMBL; AL035659; CAB62494.1; -
DR EMBL; AL035659; CAB62495.1; -
DR EMBL; AL035659; CAB62496.1; -
DR EMBL; AF188530; AAF05541.1; -
DR EMBL; AK023849; BAB14701.1; -
DR EMBL; AB028954; BAA82983.1; -
DR InterPro; IPR001440; TPR; 2.
DR InterPro; IPR000822; Znf_C2H2.
DR InterPro; IPR000571; Znf_CCCH.
DR Pfam; PF00096; zf-C2H2; 1.
DR Pfam; PF00642; zf-CCCH; 4.
DR SMART; SM00355; Znf_C2H2; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; FALSE NEG.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; FALSE NEG.
KW Nuclear protein; Repeat; Metal-binding; Zinc-finger; Coiled coil;
KW TPR repeat; Alternative splicing.
FT DOMAIN 262 357 BINDING TO NSP3.
FT DOMAIN 322 956 COILED COIL (POTENTIAL).
FT DOMAIN 982 989 POLY-ALA.
FT REPEAT 82 115 TPR 1.
FT REPEAT 116 149 TPR 2.
FT ZN_FING 501 521 C3H1-TYPE 1.
FT ZN_FING 633 651 C3H1-TYPE 2.
FT ZN_FING 776 795 C3H1-TYPE 3.
FT ZN_FING 858 882 C2H2-TYPE.
FT ZN_FING 908 927 C3H1-TYPE 4.
FT VARSPLIC 209 224 MISSING (IN ISOFORM 2).
FT CONFLICT 38 39 NL -> LE (IN REF. 4).
FT CONFLICT 88 88 R -> K (IN REF. 2).
FT CONFLICT 195 208 GTSNGLSGSIDDIET -> VGSLNPVSYIPL (IN REF. 3).
FT CONFLICT 232 232 G -> A (IN REF. 2).
FT CONFLICT 386 386 G -> V (IN REF. 2).
FT CONFLICT 676 676 S -> F (IN REF. 1; CAB62495 AND 2).
SQ SEQUENCE 993 AA; 111577 MW; B81E9E6772FFE1B CRC64;

Alignment Scores:
Pred. No.: 34.7 Length: 993
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x ROXN_HUMAN (1-993)
OY 1437 CGAGGATCCGACGACTGCTGCC 1460
Db 231 ArgglyserProAlaLeuLeuPro 238
RESULT 36
LML2_CAEL
ID LML2_CAEL STANDARD; PRT; 3672 AA.
AC Q21313;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Laminin-like protein K08C7.3 precursor.
GN K08C7.3
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Briscot N2;
RA Berks M.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC -1- SIMILARITY: CONTAINS 21.5 LAMININ EGF-LIKE DOMAINS.
```

FT DISULFID 394 403 BY SIMILARITY.
FT DISULFID 406 424 BY SIMILARITY.
FT DISULFID 427 438 BY SIMILARITY.
FT DISULFID 429 445 BY SIMILARITY.
FT DISULFID 447 456 BY SIMILARITY.
FT DISULFID 459 469 BY SIMILARITY.
FT DISULFID 472 484 BY SIMILARITY.
FT DISULFID 474 491 BY SIMILARITY.
FT DISULFID 493 502 BY SIMILARITY.
FT DISULFID 505 516 BY SIMILARITY.
FT DISULFID 519 531 BY SIMILARITY.
FT DISULFID 521 538 BY SIMILARITY.
FT DISULFID 540 549 BY SIMILARITY.
FT DISULFID 552 561 BY SIMILARITY.
FT DISULFID 566 576 BY SIMILARITY.
FT DISULFID 568 583 BY SIMILARITY.
FT DISULFID 585 594 BY SIMILARITY.
FT DISULFID 597 607 BY SIMILARITY.
FT DISULFID 610 622 BY SIMILARITY.
FT DISULFID 612 629 BY SIMILARITY.
FT DISULFID 631 640 BY SIMILARITY.
FT DISULFID 643 653 BY SIMILARITY.
FT DISULFID 656 668 BY SIMILARITY.
FT DISULFID 658 674 BY SIMILARITY.
FT DISULFID 676 685 BY SIMILARITY.
FT DISULFID 688 698 BY SIMILARITY.
FT DISULFID 701 715 BY SIMILARITY.
FT DISULFID 703 724 BY SIMILARITY.
FT DISULFID 726 735 BY SIMILARITY.
FT DISULFID 738 753 BY SIMILARITY.
FT DISULFID 756 770 BY SIMILARITY.
FT DISULFID 758 777 BY SIMILARITY.
FT DISULFID 779 788 BY SIMILARITY.
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FT DISULFID 1415 1427 BY SIMILARITY.
FT DISULFID 1417 1434 BY SIMILARITY.
FT DISULFID 1436 1445 BY SIMILARITY.
FT DISULFID 1448 1458 BY SIMILARITY.
FT DISULFID 1461 1469 BY SIMILARITY.
FT DISULFID 1463 1476 BY SIMILARITY.
FT DISULFID 1478 1487 BY SIMILARITY.
FT DISULFID 1490 1503 BY SIMILARITY.
FT DISULFID 1506 1520 BY SIMILARITY.
FT DISULFID 1508 1527 BY SIMILARITY.
FT DISULFID 1529 1538 BY SIMILARITY.
FT DISULFID 1541 1551 BY SIMILARITY.
FT DISULFID 1554 1566 BY SIMILARITY.
FT DISULFID 1556 1573 BY SIMILARITY.
FT DISULFID 1575 1584 BY SIMILARITY.
FT DISULFID 1587 1602 BY SIMILARITY.
FT DISULFID 1830 1839 BY SIMILARITY.
FT DISULFID 1832 1846 BY SIMILARITY.
FT DISULFID 1849 1858 BY SIMILARITY.
FT DISULFID 1861 1877 BY SIMILARITY.
FT DISULFID 1880 1894 BY SIMILARITY.
FT DISULFID 1882 1905 BY SIMILARITY.
FT DISULFID 1907 1916 BY SIMILARITY.
FT DISULFID 1919 1934 BY SIMILARITY.
FT DISULFID 1937 1951 BY SIMILARITY.
FT DISULFID 1939 1958 BY SIMILARITY.
FT DISULFID 1961 1970 BY SIMILARITY.
FT DISULFID 1973 1987 BY SIMILARITY.
FT DISULFID 1990 2000 BY SIMILARITY.
FT DISULFID 1992 2007 BY SIMILARITY.
FT DISULFID 2009 2018 BY SIMILARITY.
FT DISULFID 2021 2034 BY SIMILARITY.
FT DISULFID 2037 2048 BY SIMILARITY.
FT DISULFID 2039 2055 BY SIMILARITY.
FT DISULFID 2057 2066 BY SIMILARITY.
FT DISULFID 2069 2081 BY SIMILARITY.
FT DISULFID 2084 2096 BY SIMILARITY.
FT DISULFID 2086 2103 BY SIMILARITY.
FT DISULFID 2105 2114 BY SIMILARITY.

FT DISULFID 2117 2129 BY SIMILARITY.
FT CARBOHYD 121 121 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 249 249 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 351 351 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 477 477 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 511 511 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 530 530 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 634 634 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 761 761 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1014 1014 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1341 1341 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1705 1705 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1756 1756 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1868 1868 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1944 1944 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1986 1986 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2002 2002 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2159 2159 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2207 2207 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2231 2231 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2235 2235 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2401 2401 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2421 2421 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2487 2487 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2821 2821 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3087 3087 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3242 3242 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3541 3541 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 3672 AA; 404223 MW; 28E362DB5FF14BFA CRC64;

Alignment Scores:
Pred. NO.: 28.3 Length: 3672
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x LML2_CAEEL (1-3672)

OY 1142 GTATCGGAGGAGGACAGCTGCTG 1119

Db 1896 ValSerGluGlyGlnLeuLeu 1903

RESULT 37

SMS_PETMA STANDARD; PRT; 37 AA.

AC P21779;

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Somatostatin-37 (Contains: Somatostatin-34; Somatostatin-14).

OS Petromyzon marinus (Sea lamprey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hypochoarta;

OC Petromyzontiformes; Petromyzontidae; Petromyzon.

OX NCBI_TaxID-7757;

RN [1]

RP SEQUENCE.

RC TISSUE-Pancreas;

RX MEDLINE-89008497; PubMed-2902094;

RA Andrews P.C., Pollock H.G., Elliott W.M., Youson J.H.,

RA Plisetskaya E.M.;

RT "Isolation and characterization of a variant somatostatin-14 and two

RT related somatostatins of 34 and 37 residues from lamprey (Petromyzon

RL marinus).";

RL J. Biol. Chem. 263:15809-15814(1988).

CC -1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.

DR PIR; A32000; A32000. Somatostatin.

DR InterPro; IPR004250; Somatostatin.

DR Pfam; PF03002; Somatostatin; 1.

KW Cleavage on pair of basic residues; Hormone.
FT PEPTIDE 4 37 SOMATOSTATIN-34.
FT PEPTIDE 24 37 SOMATOSTATIN-14.
FT DISULFID 26 37
SQ SEQUENCE 37 AA; 4039 MW; 5918153B2775AC4D CRC64;

Alignment Scores:
Pred. No.: 546 Length: 37
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.02% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x SMS_PETWA (1-37)

QY 138 GCACGAGCTGTAGCTGGCTCC 118
|||||
Db 4 AlaAlaAlaValAlaGlySer 10

RESULT 38
6H9A_HUMAN STANDARD; PRT; 57 AA.
ID 6H9A_HUMAN
AC Q13653;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pre-T/NK cell associated protein 6H9A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Liver;
RX MEDLINE=94044805; PubMed=8228263;
RA Rames-Goldberg M.G., Hori T., Mohan-Peterson S., Spits H.;
RT "Identification of human pre-T/NK cell-associated genes.";
RL J. Immunol. 151:5810-5821(1993).
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DR EMBL: L17330; AAA16782.1;
SQ SEQUENCE 57 AA; 6068 MW; CD41EAFED2161857 CRC64;

Alignment Scores:
Pred. No.: 510 Length: 57
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.01% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x 6H9A_HUMAN (1-57)

QY 2046 AGGGTGTGTGTGGTGGT 2066
|||||

Db 32 ArgGlyValCysValleuGly 38

RESULT 39
RS27_METKA STANDARD; PRT; 73 AA.
ID RS27_METKA
AC Q8TY87;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S27E.

GN RPS27E OR RPS27A OR MK0418.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA Slesarev A.I., Mezheva K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Naitale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozlovskiy S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
and monophyly of archaeal methanogens.";
RL proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
CC - MISCELLANEOUS: Binds one zinc ion per molecule (Potential).
CC - SIMILARITY: BELONGS TO THE S27E FAMILY OF RIBOSOMAL PROTEINS.

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CC

DR EMBL: AE010337; AM01633.1;
DR PROSITE; PS01168; RIBOSOMAL_S27E; 1.
KW Ribosomal protein; Zinc-finger; Metal-binding; Complete proteome.
FT ZN_FING 28 50 C4-TYPE.
SQ SEQUENCE 73 AA; 8281 MW; FE715056D29C0E8B CRC64;

Alignment Scores:
Pred. No.: 491 Length: 73
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.02% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x RS27_METKA (1-73)

QY 1285 CAGCCACGATCTGCTTCCTC 1265
|||||

Db 18 GlnProArgSerArgPheLeu 24

RESULT 40

ID EXOX_RHISN STANDARD; PRT; 96 AA.
AC P14185;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Exopolysaccharide production repressor protein.
GN EXOX.
OS Rhizobium sp. (strain NGR234).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=90094217; PubMed=2152899;
RA Gray J.X., Djordjevic M.A., Rolfe B.G.;
RT "Two genes that regulate exopolysaccharide production in Rhizobium
sp. strain NGR234: DNA sequences and resultant phenotypes.";
RL J. Bacteriol. 172:193-203(1990).
CC - FUNCTION: INHIBITION OF EXOPOLYSACCHARIDE SYNTHESIS (EPS) AND
CC MODULATION ABILITY (NOD).
CC - PATHWAY: Exopolysaccharide biosynthesis.
CC - SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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DR EMBL; X16704; CAA34675.1;
 KW Exopolysaccharide synthesis; Nodulation; Transmembrane.
 FT TRANSMEM 6 26
 FT TRANSMEM 35 55 POTENTIAL.
 SQ SEQUENCE 96 AA; 10595 MW; A66CAF82A627D2D CRC64;

Alignment Scores:

Pred. No.: 471 Length: 96
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.01% Indels: 0
 DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x EXOX_RHISN (1-96)

QY 317 GCTTCCAGTCAGTCAGACG 337

DB 29 AlaSerThrAlaValGlnThr 35

RESULT 41

SSIC_STRHY STANDARD; PRT; 111 AA.

AC Q9R641;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Subtilisin inhibitor-like protein-12 (SIL-12) (SIL12).
 OS Streptomyces hygroscopicus.
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=1912;
 RN [1]
 RP SEQUENCE, AND CHARACTERIZATION.
 RC STRAIN=4772;
 RX MEDLINE=96176850; PubMed=8597568;
 RA Terabe M., Kojima S., Taguchi S., Momose H., Miura K.-I.;
 RT "New subtilisin-trypsin inhibitors produced by Streptomyces: primary
 RT structures and their relationship to other proteinase inhibitors from
 RT Streptomyces";
 RL Biochim. Biophys. Acta 1292:233-240(1996).
 CC -1- FUNCTION: STRONG INHIBITORY ACTIVITY TOWARD SUBTILISIN BPN' AND
 CC TO A LESSER EXTENT, TO TRYPSIN.

CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE SERINE PROTEASE INHIBITORS SSI FAMILY.

DR HSP; P01006; 3SSI.

DR InterPro; IPRO00691; Strep_subt_inhib.

DR Pfam; PF00720; SSI; 1.

DR PRINTS; PR00294; SSBTLINHSTR.

DR ProDom; PD004028; Strep_subt_inhib; 1.

DR PROSITE; PS00999; SSI; 1.

KW Serine protease inhibitor.

FT DISULFID 31 46 BY SIMILARITY.

FT DISULFID 69 99 BY SIMILARITY.

FT ACT_SITE 71 72 REACTIVE BOND (BY SIMILARITY).

SQ SEQUENCE 111 AA; 11696 MW; 608204D09C7D0376 CRC64;

Alignment Scores:

Pred. No.: 460 Length: 111
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.01% Indels: 0
 DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x SSIC_STRHY (1-111)

QY 550 ACACCCACGGCAGCCACCC 570

DB 34 ThrProThrGlyThrHisPro 40

RESULT 42

CLP3_DROME STANDARD; PRT; 112 AA.

AC P07188; Q9V4T1.

DT 01-APR-1988 (Rel. 07, Created)

DT 01-APR-1988 (Rel. 07, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Larval cuticle protein III precursor.

GN LCP3 OR CG2043.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN=Oregon-R, and Canton-S; TISSUE=Larva;

RX MEDLINE=83103095; PubMed=6817923;

RA Snyder M., Hunkapiller M., Yuen D., Silvert D., Fristrom J.,

RA Davidson N.;

RT "Cuticle protein genes of Drosophila: structure, organization and

RT evolution of four clustered genes";

RL Cell 29:1027-1040(1982).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkely;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Ananides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Zhang Q., Chen L.X.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,

RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cusley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Talali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-F., Wassarman D.A., Weinstein G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Feh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RT "The genome sequence of Drosophila melanogaster";

RL Science 287:2185-2195(2000).

CC -1- FUNCTION: COMPONENT OF THE CUTICLE OF THE LARVA OF FRUIT FLY.

CC -1- SIMILARITY: CONTAINS 1 CUTICLE CONSENSUS DOMAIN.

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CC EMBL; V00203; CAA23489.1; -
 DR EMBL; AE003837; AAF59094.1; -
 DR PIR; C25299; C25299.
 DR FlyBase; FBgn0002534; Lcp3.
 DR InterPro; IPR000618; Insect_cuticle.
 DR Pfam; PF00379; Chitin_bind_4; 1.
 DR PROSITE; PS00233; CUTICLE; 1.
 DR Structural protein; Cuticle; Signal.
 FT SIGNAL 1 16
 FT CHAIN 17 112 LARVAL CUTICLE PROTEIN III.
 FT DOMAIN 89 95 PRO-RICH.
 SQ SEQUENCE 112 AA; 11857 MW; 2C6AC731B77291A6 CRC64;

Alignment Scores:
 Pred. No.: 460 Length: 112
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.01% Indels: 0
 DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x CLP3_DROME (1-112)
 QY 1130 CCTCTCCGATACCTGCTGCC 1150
 DB 91 ProProProlleProAlaAla 97
 |||||

RESULT 43
 GV12_HALN1
 ID GV12_HALN1 STANDARD; PRT; 113 AA.
 AC Q9HHT7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE GVP1 protein 2.
 GN GVP12 OR VNG6233G.
 OS Halobacterium sp. (strain NRC-1).
 OG Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID-64091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20504483; PubMed-11016950;
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
 RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
 RA Leitch B., Keller K., Cruz R., Danson M.J., Hough D.W.,
 RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
 RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.,
 RA "Genome sequence of Halobacterium species NRC-1".
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 CC -!- FUNCTION: MAY PLAY A STRUCTURAL OR REGULATORY ROLE IN GAS
 CC VESICLE SYNTHESIS.

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 CC or send an email to license@isb-sib.ch).

CC EMBL; AE005156; AAC20889.1; -
 DR Gas vesicle; Plasmid; Complete proteome.
 SQ SEQUENCE 113 AA; 12526 MW; DEBFF803A0473E CRC64;

Alignment Scores:
 Pred. No.: 459 Length: 113
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.01% Indels: 0
 DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x GVI2_HALN1 (1-113)
 QY 583 CTCCTCCGCCAGGACTAC 603
 DB 67 LeuProAlaGlnArgThrAsn 73
 |||||

RESULT 44
 MOTI_BOVIN
 ID MOTI_BOVIN STANDARD; PRT; 115 AA.
 AC O62820;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Motilin precursor [Contains: Motilin; Motilin associated peptide
 DE (MAP)].
 GN MLN.
 OS Bos taurus (Bovine).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID-9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE-Duodenal mucosa;
 RX MEDLINE-20033565; PubMed-10564829;
 RA Huang Z., Depoortere I., De Clercq P., Peeters T.,
 RT "Sequence and characterization of cDNA encoding the motilin precursor
 RT from chicken, dog, cow and horse. Evidence of mosaic evolution in
 RT prepro-motilin.";
 RL Gene 240:217-226(1999).
 CC -!- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE REGULATION OF
 CC INTERDIGESTIVE GASTROINTESTINAL MOTILITY AND INDIRECTLY CAUSES
 CC RHYTHMIC CONTRACTION OF DUODENAL AND COLONIC SMOOTH MUSCLE (BY
 CC SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.

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CC EMBL; AF068196; AAC18864.1; -
 DR Hormone; Cleavage on pair of basic residues; Signal.
 FT SIGNAL 1 25 BY SIMILARITY.
 FT PEPTIDE 26 47 MOTILIN.
 FT PEPTIDE 50 115 MOTILIN ASSOCIATED PEPTIDE.
 SQ SEQUENCE 115 AA; 13055 MW; 017DDB70EEA5EE68 CRC64;

Alignment Scores:
 Pred. No.: 458 Length: 115
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.01% Indels: 0
 DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x MOT1_BOVIN (1-115)

QY 1679 GCACGTGCTCTCTCTCTGGCT 1699

Db 6 AlathraAlaValLeuLeuAla 12

RESULT 45

YD5_SCHPO

ID YD5_SCHPO STANDARD; PRT; 115 AA.

AC Q10493;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Very hypothetical protein C26F1.05 in chromosome I.

GN SPAC26F1.05.

OS Schizosaccharomyces pombe (Fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OX NCBI_TaxID=4896;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=972;

RX MEDLINE=2184801; PubMed=11859360;

RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jageis K.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Voiclaert G., Aert R., Robben J., Grymonprez B.,

RA Weijtens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Calbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,

RT "The genome sequence of Schizosaccharomyces pombe";

RL Nature 415:871-880(2002).

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DR EMBL; Z73100; CAA97362.1; --

KW Hypothetical protein.

SQ SEQUENCE 115 AA; 13477 MW; B0C842741F30326D CRC64;

Alignment Scores:

Pred. No.:	458	Length:	115
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.01%	Indels:	0
DB:	1	Gaps:	0

US-09-824-647-16 (1-2095) x YD5_SCHPO (1-115)

QY 1122 CACGTGCTCTCTCTCTCGATAC 1142

Db 22 GlnLeuSerLeuLeuArgTyr 28

Search completed: July 7, 2003, 16:02:08
Job time : 75 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: July 7, 2003, 15:47:40 ; Search time 159.5 Seconds

(without alignments)
5412.774 Million cell updates/sec

Title: US-09-824-647-16

Perfect score: 694

Sequence: 1 cgcaggcagaccatgtggac.....ataaagttgtcactttctt 2095

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 671580 seqs, 206047115 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1343044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-O-/cgn2.1/USPTO.spool/US09824647/runat_07072003_154718_26035/app_query.fasta_1.2247
-DB-SPREMBL_21 -QWTF-fastan -SUFFIX-std.rspt -MINMATCH=0.1 -LOOPCL=0
-LIST=45 -UNITS-bits -START=1 -END=1 -MATRIX-oligo -TRANS-human40.cdl
-OUTFT-pto -NORM-ext -HEAPSZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER-US09824647.ecgn_1.1.231.runat_07072003_154718_26035 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DRV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_prodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	155	22.3	413	4	Q9H8S1	Q9H8S1 homo sapien

ID	Q9H8S1	PRELIMINARY	PRT	413 AA
AC	Q9H8S1			
DT	01-MAR-2001 (TrEMBLrel. 16, Created)			
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DE	OVARC1001154 protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-OVARIAN CARCINOMA;			
RA	Isoqai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,			
RA	Nishikawa T., Nagai K., Sato H., Sugano S., Shiratori A., Sudo H.,			
RA	Wakatsuna M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,			
RA	Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,			
RA	Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,			
RA	Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y.,			
RA	Ninomiya K., Iwayanagi T.,			
RT	*NEDO human cDNA sequencing project.*;			
RL	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK023348; BAB14535.1; -			

ALIGNMENTS

RESULT 1.

ID	Q9H8S1	PRELIMINARY	PRT	413 AA
AC	Q9H8S1			
DT	01-MAR-2001 (TrEMBLrel. 16, Created)			
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DE	OVARC1001154 protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-OVARIAN CARCINOMA;			
RA	Isoqai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,			
RA	Nishikawa T., Nagai K., Sato H., Sugano S., Shiratori A., Sudo H.,			
RA	Wakatsuna M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,			
RA	Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,			
RA	Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,			
RA	Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y.,			
RA	Ninomiya K., Iwayanagi T.,			
RT	*NEDO human cDNA sequencing project.*;			
RL	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK023348; BAB14535.1; -			

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.
RA Kuehl P., Lewis S., Matsuo Y., Nkaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Humé D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasakura H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RT *Functional annotation of a full-length mouse cDNA collection.*;
RL Nature 409:685-690(2001).
DR EMBL; AKO18744; BAB31384.1; -
DR MGD; MGI:95832; Grn.
DR InterPro; IPR000118; Granulin.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00396; granulin; 7.
DR SMART; SM00277; GRAN; 7.
DR PROSITE; PS00799; GRANULINS; 7.
DR PROSITE; PS00118; PA2_HIS; UNKNOWN 1.
SQ SEQUENCE 589 AA; 63405 MW; 1DE8229C413CA292 CRC64;

Alignment Scores:
Pred. No.: 1.39e-22 Length: 589
Score: 32.00 Matches: 32
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.61% Indels: 0
DB: 11 Gaps: 0

US-09-824-647-16 (1-2095) x Q9D2V3 (1-589)

QY 1396 GGGAGCTGGGCTGTGCCAGTTCGCCATGCTGTGCTGCGGAGGATCCGCACACTGC 1455
|||||
Db 460 GlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHisCys 479
|||

QY 1456 TGCCCGCTGGCTACACCTGCAACCTGAAGGCTCGA 1491
|||||
Db 480 CysProAlaGlyTrpThrCysAsnValLysAlaArg 491
|||||

RESULT 3
ID Q9DWB4 PRELIMINARY; PRT: 51 AA.
AC Q9DWB4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE PC cell-derived growth factor, PCDGF-EPIHELIN precursor homolog
DE (Fragments).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE
RX MEDLINE=93266526; PubMed=8496151;
RA Zhou J., Gao G., Crabbs J.W., Serrero G.;
RT "Purification of an autocrine growth factor homologous with mouse
epithelin precursor from a highly tumorigenic cell line.";
RL J. Biol. Chem. 268:10863-10869(1993).
FT NON_TER 1 1
FT NON_CONS 29 30
FT NON_TER 51 51
SQ SEQUENCE 51 AA; 5473 MW; C349143E4E942AF CRC64;

Alignment Scores:
Pred. No.: 18.6 Length: 51
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0

DR InterPro; IPR000118; Granulin.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00396; granulin; 4.
DR SMART; SM00277; GRAN; 4.
DR PROSITE; PS00799; GRANULINS; UNKNOWN 4.
DR PROSITE; PS00118; PA2_HIS; UNKNOWN 1.
SQ SEQUENCE 413 AA; 44132 MW; 0E3767A44BE314EC CRC64;

Alignment Scores:
Pred. No.: 1.15e-145 Length: 413
Score: 155.00 Matches: 155
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 22.33% Indels: 0
DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x Q9HBS1 (1-413)

QY 766 GTGTGTACCTGATCCAGTAGTAAGTGCTCTCCAAGGAGAAGCGTACCAGGACCTCTCTC 825
|||||
Db 72 ValCysAspLeuIleGlnSerLysCysLeuSerLysGluAsnAlaThrThraspLeuLeu 91
|||||

QY 826 ACTAGTCTGCTGCCACACAGTGGCGGATGTGAATGTGACATGGAGGTGACCTGCCCA 885
|||||
Db 92 ThrLysLeuProAlaHisThrValGlyAspValLysCysAspMetGluValSerCysPro 111
|||||

QY 886 GATGCTATACCTGCTGCGCTACAGTCGAGCGGGGCTGCTGCCCTTTTACCAG 945
|||||
Db 112 AspGlyThrCysCysArgLeuGlnSerGlyAlaTrpGlyCysCysProPheThrGln 131
|||||

QY 946 GCTGTGCTGTGAGACACATACATGCTGCTCCGCGGGGTTTACGTGTGACAGCAG 1005
|||||
Db 132 AlaValCysCysGluAspHisIleHisCysCysProAlaGlyPheThrCysAspThrGln 151
|||||

QY 1006 AAGGTACTGTGAACAGAGGGCCCCACAGTGGCTGGATGGAGAGAGGCCGCCAGCTCAC 1065
|||||
Db 152 LysGlyThrCysGluGlnGlyProHisGlnValProTrpMetGluLysAlaProAlaHis 171
|||||

QY 1066 CTCAGCTCCAGACCCACAGCCTTGAAGAGATGTCCTGTGATAATGTGACAGCAG 1125
|||||
Db 172 LeuSerLeuProAspProGlnAlaLeuLysArgaspValProCysAspAsnValSerSer 191
|||||

QY 1126 TGTCCCTCTCCGATACCTGCTGCCAACTACGCTGCGGGAGTGGGCTGTGTCCTCAATC 1185
|||||
Db 192 CysProSerSerAspThrCysCysGlnLeuThrSerGlyGluTrpGlyCysCysProIle 211
|||||

QY 1186 CCAGAGCTGTGCTGCTGCGACACACAGCAGTCTGCTGCCCCCGAG 1230
|||||
Db 212 ProGluAlaValCysCysSerAspHisGlnHisCysCysProGln 226
|||||

RESULT 2
ID Q9D2V3 PRELIMINARY; PRT: 589 AA.
AC Q9D2V3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Adult male kidney cDNA, RIKEN full-length enriched library,
DE clone:0610012H06, full insert sequence.
GN GRN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RP RP

Query Match: 1.30% Indels: 0
DB: 11 Gaps: 0

US-09-824-647-16 (1-2095) x Q9QWB4 (1-51)

QY 811 ACCACGACCTCTCAGTGGCT 837

DB 36 ThrThrAspLeuLeuThrLysLeuPro 44

RESULT 4

Q9X402 PRELIMINARY; PRT; 266 AA.

AC Q9X402

DT 01-NOV-1999 (TReMBLrel. 12, Created)

DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)

DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)

DE Putative ABC transporter membrane-associated protein (Fragment).

GN MSNF

OS Methylosulfonomonas methylovora.

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Methylosulfonomonas.

OX NCBI_TaxID=50057;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=M2;

RA MEDLINE=99194735; PubMed=10094704;

RA De Marco P., Moradas-Ferreira P., Higgins T.P., McDonald I.,

RA Kenna E.M., Murrell J.C.;

RT "Molecular analysis of a novel methanesulfonic acid monooxygenase from

RT the methylophilic Methylosulfonomonas methylovora.,"

RL J. Bacteriol. 181:2244-2251(1999).

DR EMBL; AF091716; AAD26617.1; -

FT NCBI_TaxID=50057;

FT NCBI_TaxID=50057;

SQ SEQUENCE 266 AA; 29281 MW; 2AFAEDC02B575010 CRC64;

Alignment Scores:

Pred. No.: 15.7 Length: 266

Score: 9.00 Matches: 9

Percent Similarity: 100.00% Conservativity: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.30% Indels: 0

DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x Q9X402 (1-266)

QY 1617 AGACACCGACAGGCTGGCGCTG 1643

DB 21 ArgGlnProThrGlyLeuGlyLeuLeu 29

RESULT 5

Q8VUF4

AC Q8VUF4 PRELIMINARY; PRT; 355 AA.

DT 01-MAR-2002 (TReMBLrel. 20, Created)

DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

DE 6-hydroxycyclohex-1-ene-1-carboxyl-CoA dehydrogenase.

GN B2DX.

OS Azoroccus evansii.

OC Bacteria; Proteobacteria; beta subdivision; Rhodocyclus group;

OC Azoroccus.

OX NCBI_TaxID=59406;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=K9740;

RA Mohr K., Herrmann H., Burchhardt G.;

RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ428529; CAD21637.1; -

DR InterPro; IPR002085; Adh_zn_family.

DR InterPro; IPR000345; CytC_heme_bind.

DR Pfam; PF00107; adh_zinc; 1.

DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.

SQ SEQUENCE 355 AA; 38211 MW; 5E1D930131F800A6 CRC64;

Alignment Scores:

Pred. No.: 15.3 Length: 355

Score: 9.00 Matches: 9

Percent Similarity: 100.00% Conservativity: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.31% Indels: 0

DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x Q8VUF4 (1-355)

QY 741 GTCATCGGACGACGAGTGGCTGGG 715

DB 173 ValIleGlyAlaAlaGlyGlyValGly 181

RESULT 6

Q8Y2X4

ID Q8Y2X4 PRELIMINARY; PRT; 408 AA.

AC Q8Y2X4

DT 01-MAR-2002 (TReMBLrel. 20, Created)

DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

DE Putative transporter transmembrane protein.

GN RSC0207 OR RS00639.

OS Ralstonia solanacearum (Pseudomonas solanacearum).

OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;

OC Ralstonia.

OX NCBI_TaxID=305;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GM1000;

RA MEDLINE=21681879; PubMed=11823852;

RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,

RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., N.,

RA Gaspin C., Choise N., Claudel-Renard C., Cunnac S., Demange N.,

RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,

RA Weissbach J., Boucher C.A.;

RT "Genome sequence of the plant pathogen Ralstonia solanacearum.,"

RL Nature 415:497-502(2002)

DR EMBL; AL646058; CAD13735.1; -

DR InterPro; IPR003662; sub_transporter.

DR Pfam; PF00083; sugar_tr; 1.

KW Complete proteome.

SQ SEQUENCE 408 AA; 41634 MW; 2F9943B095187FC0 CRC64;

Alignment Scores:

Pred. No.: 15.1 Length: 408

Score: 9.00 Matches: 9

Percent Similarity: 100.00% Conservativity: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.31% Indels: 0

DB: 16 Gaps: 0

US-09-824-647-16 (1-2095) x Q8Y2X4 (1-408)

QY 1458 GCACGAGTGGCGATCCCTCGCAGCA 1432

DB 386 AlaAlaValleuAlaIleuAlaAa 394

RESULT 7

P74015

ID P74015 PRELIMINARY; PRT; 633 AA.

AC P74015

DT 01-FEB-1997 (TReMBLrel. 02, Created)

DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)

DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

DE Sensory transduction histidine kinase.

GN SL11228.

OS Synechocystis sp. (strain PCC 6803).

OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.

OX NCBI_TaxID=1148;

RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE-97061201; PubMed-8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirose M., Sugitani M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimpō S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 CC -1- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
 CC REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
 CC -1- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.
 CC EMBL; D90911; BA018086.1; --
 DR HSSP; P10957; IRLN.
 DR InterPro; IPR003594; ATPbind_ATPase.
 DR InterPro; IPR004358; Bact_sens_pr_C.
 DR InterPro; IPR003018; GAF.
 DR InterPro; IPR003661; His_kinA.
 DR InterPro; IPR004359; HIS_KIN_sig.
 DR InterPro; IPR001789; Response_reg.
 DR Pfam; PF01590; GAF; 1.
 DR Pfam; PF00072; response_reg; 1.
 DR Pfam; PF00512; signal; 1.
 DR PRINTS; PR00344; BCTRLSENSOR.
 DR ProDom; PD000039; Response_reg; 1.
 DR SMART; SM00065; GAF; 1.
 DR SMART; SM00387; HATPase_c; 1.
 DR SMART; SM00388; Hiska; 1.
 DR SMART; SM00448; REC; 1.
 KW Kinase; Phosphorylation; Sensory transduction; Transferase;
 KW Complete proteome.
 SQ SEQUENCE 633 AA; 69896 MW; 2128D1E7D56F33C1 CRC64;

Alignment Scores:
 Pred. No.: 14.4 Length: 633
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.30% Indels: 0
 DB: 16 Gaps: 0

US-09-824-647-16 (1-2095) x P74015 (1-633)
 QY 1322 CCCACCCGAGACATCGCTGTGACC 1348
 Db 401 ProThrProGluThrSerAlaValThr 409
 |||||
 RESULT 8
 O18414 PRELIMINARY; PRT; 1191 AA.
 AC O18414;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Zinc-finger protein USH (U-shaped protein).
 GN USH OR CG2762.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-EMBRYO;
 RX MEDLINE-98037748; PubMed-9367989;
 RA Cubadda Y., Heitzler P., Ray R.P., Bourouis M., Raman P., Gelbart W.,
 RA Simpson P., Haenlin M.;
 RT "u-shaped encodes a zinc finger protein that regulates the proneural
 RT genes achaete and scute during the formation of bristles in
 RT Drosophila.";

RL Genes Dev. 11:3083-3095(1997).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; Y12322; CAA72991.1; --
 DR FlyBase; FBgn0003963; ush.
 DR InterPro; IPR000822; znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 8.
 DR PRINTS; PR00048; ZINC_FINGER.
 DR SMART; SM00355; znf_C2H2; 6.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
 KW DNA-binding; Nuclear protein; Zinc-finger.
 SQ SEQUENCE 1191 AA; 124561 MW; C4C599C690C7096B CRC64;

Alignment Scores:
 Pred. No.: 13.5 Length: 1191
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.31% Indels: 0
 DB: 5 Gaps: 0

US-09-824-647-16 (1-2095) x O18414 (1-1191)
 QY 138 GCACGAGCTGTAGCTGCTCTCGGG 112
 Db 679 AlaAlaValAlaGlySerSerGly 687
 |||||
 RESULT 9
 Q26835 PRELIMINARY; PRT; 17 AA.
 ID Q26835;
 AC Q26835;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE (Iratat 2.4) variant surface glycoprotein TC gene (Fragment).
 OS Trypanosoma brucei.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5691;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-86278091; PubMed-2942540;
 RA Brown K.H., Brentano S.F., Donelson J.E.;
 RT "Mung bean nuclease cleaves preferentially at the boundaries of
 RT variant surface glycoprotein gene transpositions in trypanosome DNA.";
 RL J. Biol. Chem. 261:10352-10358(1986).
 DR EMBL; M14022; AAA30308.1; --
 FT NON_TER 1
 SQ SEQUENCE 17 AA; 1783 MW; 4A20FB55CF59E5B CRC64;

Alignment Scores:
 Pred. No.: 208 Length: 17
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.16% Indels: 0
 DB: 5 Gaps: 0

US-09-824-647-16 (1-2095) x Q26835 (1-17)
 QY 1632 GCCCTGCTGCTGCTGCTCGGACCA 1609
 Db 4 AlaLeuSerValValSerAlaAla 11
 |||||
 RESULT 10
 Q98KE0 PRELIMINARY; PRT; 48 AA.
 ID Q98KE0;
 AC Q98KE0;
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypothetical protein ms11520.
 GN MS11520.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Phyllobacteriaceae; Mesorhizobium.
 RN NCBI_TaxID=381;
 RP [1]
 RC SEQUENCE FROM N.A.
 RX STRAIN-WAF303099;
 RA MEDLINE-21082930; PubMed-11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Iidesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti";
 RL DNA Res. 7:331-338(2000).
 DR EMBL; AF002997; BAB48874.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 48 AA; 5437 MW; 37A2002130817620 CRC64;

Alignment Scores:
 Pred. No.: 187 Length: 48
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.16% Indels: 0
 DB: 16 Gaps: 0

US-09-824-647-16 (1-2095) x Q98KE0 (1-48)

QY 1310 CGCGGGCAGGCATCTCTCCACT 1287

Db 3 ArgArgAlaGlyIlePheSer 10

RESULT 11

Q26763 ID Q26763 PRELIMINARY; PRT; 59 AA.
 AC Q26763;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Trypanosoma brucei variable surface antigen 1.8 mRNA 3'-end
 DE (Fragment).
 OS Trypanosoma brucei.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5691;
 RN [1]
 RX MEDLINE-84261425; PubMed-6086319;
 RA Michels P.A.M., van der Ploeg L.H.T., Liu A.Y.C., Borst P.;
 RT "The inactivation and reactivation of an expression-linked gene copy
 RT for a variant surface glycoprotein in Trypanosoma brucei";
 RL EMBO J. 3:1345-1351(1984).
 DR EMBL; X00625; CAA25259.1; -;
 FT NON_TER 1 1
 SQ SEQUENCE 59 AA; 6642 MW; 9CDD30CFA24461E8 CRC64;

Alignment Scores:
 Pred. No.: 184 Length: 59
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.16% Indels: 0
 DB: 5 Gaps: 0

US-09-824-647-16 (1-2095) x Q26763 (1-59)

QY 1632 GCCTGTGCTGCTCTCCAGCA 1609

Db 46 AlaLeuSerValSerAlaLa 53

RESULT 12

Q26036 ID Q26036 PRELIMINARY; PRT; 68 AA.
 AC Q26036;

DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Variable surface antigen (Fragment).
 OS Trypanosoma brucei.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5691;
 RN [1]
 RX SEQUENCE FROM N.A.
 RX MEDLINE-84242548; PubMed-6737319;
 RA Murphy W.J., Brentano S.T., Rice-Ficht A.C., Dorfman D.M.,
 RA Donelson J.E.;
 RT "DNA rearrangements of the variable surface antigen genes of the
 RT Trypanosomes";
 RL J. Protozool. 31:65-73(1984).
 DR EMBL; M31538; AAA30294.1; -;
 FT NON_TER 1 1
 SQ SEQUENCE 68 AA; 7641 MW; 388437A80C8F5266 CRC64;

Alignment Scores:
 Pred. No.: 181 Length: 68
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.16% Indels: 0
 DB: 5 Gaps: 0

US-09-824-647-16 (1-2095) x Q26036 (1-68)

QY 1632 GCCTGTGCTGCTCTCCAGCA 1609

Db 55 AlaLeuSerValSerAlaLa 62

RESULT 13

Q9B134 ID Q9B134 PRELIMINARY; PRT; 93 AA.
 AC Q9B134;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE NADH dehydrogenase subunit 2 (Fragment).
 DE Cyprinella lutrensis (red shiner).
 OS Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinella.
 OX NCBI_TaxID=28791;
 RN [1]
 RX SEQUENCE FROM N.A.
 RC STRAIN-1, AND 2;
 RA Grose M.J., Wiley E.O.;
 RT "Phylogenetic relationships of the Hybopsis amblops species group
 RT (Teleostei: Cyprinidae).";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE -> NAD(+) + UBIQUINOL.
 DR EMBL; AF216598; AAK34889.1; -;
 DR EMBL; AF216590; AAK34891.1; -;
 DR InterPro; IPR001750; Oxidored_q1.
 DR Pfam; PF00361; oxidored_q1; 1.
 KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
 FT NON_TER 1 1
 SQ SEQUENCE 93 AA; 10071 MW; AOC6713C0C0B3879 CRC64;

Alignment Scores:
 Pred. No.: 175 Length: 93
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.15% Indels: 0
 DB: 8 Gaps: 0

US-09-824-647-16 (1-2095) x Q9B134 (1-93)

RC TISSUE-BRAIN;
MEDLINE-96207227; PubMed-8619474;
RA Andersson B., Wentland M.A., Ricafrete J.Y., Liu W., Gibbs R.A.;
RT "A 'double adaptor' method for improved shotgun library
construction.";
RL Anal. Biochem. 236:107-113(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-97264341; PubMed-9110174;
RY Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W.,
RZ Ricafrete J.Y., Wentland M.A., Lennon G., Gibbs R.A.;
SA "Large-scale concatenation cDNA sequencing.";
SB Genome Res. 7:353-358(1997).
SC EMBL; AF035293; AAB88180.1;
SD InterPro; IPR003140; PLP_Cesterase.
SE Pfam; PF02230; abhydrolase_2; 1.
SF NON_TER 1
SQ SEQUENCE 104 AA; 11403 MW; CE6C320EEA1011B3 CRC64;

Alignment Scores:
Pred. No.: 173 Length: 104
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x 043202 (1-104)
QY 1686 CTTGCTGTCTGGTTCGCCGTGC GC 1709
Db 16 LeuSerCysTrpLeuProLeuArg 23
RESULT 16
O07154 PRELIMINARY; PRT; 111 AA.
AC O07154;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE Hypothetical 12.2 kDa protein.
GS MCL581.20.
OS Mycobacterium leprae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RA Oliver K., Harris D.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-93188700; PubMed-8446027;
RY Eaglemeier K., Honore N., Woods S.A., Caudron B., Cole S.T.;
SZ "Use of an ordered cosmid library to deduce the genomic organization
of Mycobacterium leprae.";
TL Mol. Microbiol. 7:197-206(1993).
DR EMBL; Z96801; CAB09641.1;
KW Hypothetical protein.
SQ SEQUENCE 111 AA; 12241 MW; 13DD36663FDF0B8C CRC64;

Alignment Scores:
Pred. No.: 172 Length: 111
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 2 Gaps: 0

RC TISSUE-BRAIN;
MEDLINE-96207227; PubMed-8619474;
RA Andersson B., Wentland M.A., Ricafrete J.Y., Liu W., Gibbs R.A.;
RT "A 'double adaptor' method for improved shotgun library
construction.";
RL Anal. Biochem. 236:107-113(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-97264341; PubMed-9110174;
RY Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W.,
RZ Ricafrete J.Y., Wentland M.A., Lennon G., Gibbs R.A.;
SA "Large-scale concatenation cDNA sequencing.";
SB Genome Res. 7:353-358(1997).
SC EMBL; AF035293; AAB88180.1;
SD InterPro; IPR003140; PLP_Cesterase.
SE Pfam; PF02230; abhydrolase_2; 1.
SF NON_TER 1
SQ SEQUENCE 104 AA; 11403 MW; CE6C320EEA1011B3 CRC64;

Alignment Scores:
Pred. No.: 173 Length: 104
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x 043202 (1-104)
QY 1686 CTTGCTGTCTGGTTCGCCGTGC GC 1709
Db 16 LeuSerCysTrpLeuProLeuArg 23
RESULT 16
O07154 PRELIMINARY; PRT; 111 AA.
AC O07154;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE Hypothetical 12.2 kDa protein.
GS MCL581.20.
OS Mycobacterium leprae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RA Oliver K., Harris D.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-93188700; PubMed-8446027;
RY Eaglemeier K., Honore N., Woods S.A., Caudron B., Cole S.T.;
SZ "Use of an ordered cosmid library to deduce the genomic organization
of Mycobacterium leprae.";
TL Mol. Microbiol. 7:197-206(1993).
DR EMBL; Z96801; CAB09641.1;
KW Hypothetical protein.
SQ SEQUENCE 111 AA; 12241 MW; 13DD36663FDF0B8C CRC64;

Alignment Scores:
Pred. No.: 172 Length: 111
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 2 Gaps: 0

RC TISSUE-BRAIN;
MEDLINE-96207227; PubMed-8619474;
RA Andersson B., Wentland M.A., Ricafrete J.Y., Liu W., Gibbs R.A.;
RT "A 'double adaptor' method for improved shotgun library
construction.";
RL Anal. Biochem. 236:107-113(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-97264341; PubMed-9110174;
RY Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W.,
RZ Ricafrete J.Y., Wentland M.A., Lennon G., Gibbs R.A.;
SA "Large-scale concatenation cDNA sequencing.";
SB Genome Res. 7:353-358(1997).
SC EMBL; AF035293; AAB88180.1;
SD InterPro; IPR003140; PLP_Cesterase.
SE Pfam; PF02230; abhydrolase_2; 1.
SF NON_TER 1
SQ SEQUENCE 104 AA; 11403 MW; CE6C320EEA1011B3 CRC64;

Alignment Scores:
Pred. No.: 173 Length: 104
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x 043202 (1-104)
QY 1686 CTTGCTGTCTGGTTCGCCGTGC GC 1709
Db 16 LeuSerCysTrpLeuProLeuArg 23
RESULT 16
O07154 PRELIMINARY; PRT; 111 AA.
AC O07154;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE Hypothetical 12.2 kDa protein.
GS MCL581.20.
OS Mycobacterium leprae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RA Oliver K., Harris D.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-93188700; PubMed-8446027;
RY Eaglemeier K., Honore N., Woods S.A., Caudron B., Cole S.T.;
SZ "Use of an ordered cosmid library to deduce the genomic organization
of Mycobacterium leprae.";
TL Mol. Microbiol. 7:197-206(1993).
DR EMBL; Z96801; CAB09641.1;
KW Hypothetical protein.
SQ SEQUENCE 111 AA; 12241 MW; 13DD36663FDF0B8C CRC64;

Alignment Scores:
Pred. No.: 172 Length: 111
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 2 Gaps: 0

RC TISSUE-BRAIN;
MEDLINE-96207227; PubMed-8619474;
RA Andersson B., Wentland M.A., Ricafrete J.Y., Liu W., Gibbs R.A.;
RT "A 'double adaptor' method for improved shotgun library
construction.";
RL Anal. Biochem. 236:107-113(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-97264341; PubMed-9110174;
RY Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W.,
RZ Ricafrete J.Y., Wentland M.A., Lennon G., Gibbs R.A.;
SA "Large-scale concatenation cDNA sequencing.";
SB Genome Res. 7:353-358(1997).
SC EMBL; AF035293; AAB88180.1;
SD InterPro; IPR003140; PLP_Cesterase.
SE Pfam; PF02230; abhydrolase_2; 1.
SF NON_TER 1
SQ SEQUENCE 104 AA; 11403 MW; CE6C320EEA1011B3 CRC64;

Alignment Scores:
Pred. No.: 173 Length: 104
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x 043202 (1-104)
QY 1686 CTTGCTGTCTGGTTCGCCGTGC GC 1709
Db 16 LeuSerCysTrpLeuProLeuArg 23
RESULT 16
O07154 PRELIMINARY; PRT; 111 AA.
AC O07154;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL

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US-09-824-647-16 (1-2095) x 007154 (1-111)
QY 1392 CTGGCTCGGCGACGAGTTCGCC 1369
Db 15 LeuAlaArgAlaAlaGlySerAla 22

RESULT 17
Q915P6 PRELIMINARY; PRT; 143 AA.
ID AC Q915P6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Hypothetical protein PA0679.
GN PA0679.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Raizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
KW EMBL; AB004503; AAG04068.1; --
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 143 AA; 15028 MW; 0235C5E9CEDC3DD CRC64;

Alignment Scores:
Pred. No.: 168 Length: 143
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 16 Gaps: 0

US-09-824-647-16 (1-2095) x Q915P6 (1-143)
QY 1458 GCAGCAGTCTGGCGATCCTCGCA 1435
Db 16 AlaAlaValLeuAlaAlaLeuAla 23

RESULT 18
Q9X549 PRELIMINARY; PRT; 149 AA.
ID AC Q9X549;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE YagLD.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Plasmid R-plasmid pAG1.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Corynebacteriaceae;
OC Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=22243;
RX MEDLINE=20532766; PubMed=11078655;
RA Tauch A., Puhler A., Kallinowski J., Thierbach G.;
RA "YagLD, a New Tetracycline Resistance Determinant Discovered in Gram-
RT Positive Bacteria, Shows High Homology to Gram-Negative Regulated
RT Efflux Systems.";

plasmid 44:285-291(2000).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=22243;
RA Tauch A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AF121000; AAD25068.1;
DR InterPro; IPR003795; DUF192.
DR Pfam; PF02643; DUF192; 1.
KW Plasmid.
SQ SEQUENCE 149 AA; 15897 MW; 398307CEE67DA4D CRC64;

Alignment Scores:
Pred. No.: 167 Length: 149
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x Q9X549 (1-149)
QY 110 ACCCGGAGGAGCGACGCTACAGCT 133
Db 21 ThrProGluProAlaThrAla 28

RESULT 19
Q916W2 PRELIMINARY; PRT; 154 AA.
ID AC Q916W2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Genome polyprotein [Contains: envelope glycoprotein E2 (GP68) (GP70)
DE (NS1)] (Fragment).
DE Hepatitis C virus.
OS Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=ACL-92;
RA Lyra A.C., Fan X., Di Bisceglie A.M.;
RT "Evolution of hepatitis C viral quasiespecies after liver
RT transplantation.";
CC -1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
DR EMBL; AF422337; AAL24649.1;
DR InterPro; IPR002519; HCV_env.
DR InterPro; IPR002531; HCV_NS1.
DR Pfam; PF01539; HCV_env; 1.
DR Pfam; PF01560; HCV_NS1; 1.
DR ProDom; PD186062; HCV_NS1; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 154
SQ SEQUENCE 154 AA; 16728 MW; CAF5DA7B61F6C48A CRC64;

Alignment Scores:
Pred. No.: 167 Length: 154
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 12 Gaps: 0

US-09-824-647-16 (1-2095) x Q916W2 (1-154)
QY 1196 TCTGCTCGGACGACGACGCT 1219
Db 106 SerAlaAlaArgThrSerThr 113
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RESULT 20
Q8Q0M8 ID Q916W1 PRELIMINARY; PRT; 154 AA.
AC Q916W1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Genome polyprotein [Contains: envelope glycoprotein E2 (GP68) (GP70)
DE (NS1)] (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ACL-93;
RA Lyra A.C., Fan X., Di Bisceglie A.M.;
RT "Evolution of hepatitis C viral quasiespecies after liver
RT transplantation."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
DR EMBL; AF422338; AAL24650.1; -
DR InterPro; IPR002519; HCV_env.
DR Pfam; PF01539; HCV_env; 1.
DR Pfam; PF01560; HCV_NSI; 1.
DR ProDom; PD186062; HCV_NSI; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 154 154
SQ SEQUENCE 154 AA; 16756 MW; C4F5DA7B61E44F84 CRC64;

Alignment Scores:
Pred. No.: 167 Length: 154
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 12 Gaps: 0

US-09-824-647-16 (1-2095) x Q916W1 (1-154)
QY 1196 TCTGCTGCTCGGACCACT 1219
DB 106 SerAlaAlaArgThrSerThr 113

RESULT 21
Q8Q0M8 ID Q8Q0M8 PRELIMINARY; PRT; 154 AA.
AC Q8Q0M8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E1/E2 protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ACL-292;
RA Lyra A.C., Fan X., Di Bisceglie A.M.;
RT "Evolution of hepatitis C viral quasiespecies after liver
RT transplantation."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF497310; AAM19566.1; -
DR NON_TER 1 1
DR NON_TER 154 154
SQ SEQUENCE 154 AA; 16713 MW; 3592CC16C3BFEF15 CRC64;

Alignment Scores:
Pred. No.: 167 Length: 154
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 12 Gaps: 0

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Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 12 Gaps: 0

US-09-824-647-16 (1-2095) x Q8Q0M8 (1-154)
QY 1196 TCTGCTGCTCGGACCACT 1219
DB 106 SerAlaAlaArgThrSerThr 113

RESULT 22
Q84305 ID Q84305 PRELIMINARY; PRT; 171 AA.
AC Q84305;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein CT303.
GN CT303.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-D/UW-3/CX;
RX MEDLINE-99000809; PubMed-9784136;
RA Stephens R.S., Kaiman S., Lammell C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis."
RL Science 282:754-759(1998).
KW EMBL; AE001303; AAC67896.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 171 AA; 19423 MW; 3CB88DD2D08B24BF CRC64;

Alignment Scores:
Pred. No.: 165 Length: 171
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 16 Gaps: 0

US-09-824-647-16 (1-2095) x Q84305 (1-171)
QY 1125 CTGTCCTCTCGGACCACT 1148
DB 11 LeuSerLeuLeuArgTyrLeuLeu 18

RESULT 23
Q9PK90 ID Q9PK90 PRELIMINARY; PRT; 178 AA.
AC Q9PK90;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein TC0577.
GN TC0577.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MOPN / NIGG;
RX MEDLINE-20150255; PubMed-10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Uitterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;

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RT *Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
 RL pneumoniae AK39.*; 28:1397-1406(2000).
 DR Nucleic Acids Res. 28:1397-1406(2000).
 DR EMBL; AE002326; AAF39412.1;
 KW TIGR; TC0577;
 DR Hypothetical protein; Complete proteome.
 SQ SEQUENCE 178 AA; 20384 MW; 5D11D1EA77B3DE39 CRC64;

Alignment Scores:
 Pred. No.: 164 Length: 178
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.15% Indels: 0
 DB: 16 Gaps: 0

US-09-824-647-16 (1-2095) x Q9PK90 (1-178)

OY 1125 CTGTCCTCGCTCGATACCTGCG 1148
 |||||
 Db 18 LeuSerLeuLeuArgTyrLeuLeu 25

RESULT 24

O8XX13 PRELIMINARY; PRT; 188 AA.

AC O8XX13; 2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Probable transmembrane protein.
 GN RSC2305 OR RS01247.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
 OC Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-GH11000;
 RX MEDLINE-21681879; PubMed-11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Arlat M., Billault A., Brottier P., Camus J.C., Catolico L.,
 RA Chandler M., Choise N., Claudel-Renard C., Cunac S., Demange N.,
 RA Siquier P., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 RA Weissbach J., Thebault P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RT *Genome sequence of the plant pathogen Ralstonia solanacearum.*;
 RL Nature 415:497-502(2002).
 DR EMBL; AL646069; CAD16012.1;
 DR InterPro; IPR000104; Antifreeze_1.
 DR PRINTS; PR00308; ANTIFREEZE1.
 KW Complete proteome.
 SQ SEQUENCE 188 AA; 20087 MW; FE91790FB88B3649 CRC64;

Alignment Scores:
 Pred. No.: 163 Length: 188
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.15% Indels: 0
 DB: 16 Gaps: 0

US-09-824-647-16 (1-2095) x Q8XX13 (1-188)

OY 1454 GTGCCCGCTGCTACACCTGCA 1477
 |||||
 Db 37 AlaAlaArgLeuAlaThrProAla 44

RESULT 25

Q8QS62 PRELIMINARY; PRT; 190 AA.

ID Q8QS62
 AC Q8QS62;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Regument protein UL26.
 OS Chimpanzee cytomegalovirus.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Cytomegalovirus.
 OX NCBI_TaxID=188763;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Davison A.J., Akter P., Dolan A., Wright K.M., Addison C.,
 RA Alcendor D.J., Hayward G.S., McGeoch D.J.;
 RT *The human cytomegalovirus genome revisited.*;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF480884; AAM00677.1;
 SQ SEQUENCE 190 AA; 21528 MW; E918F4FC02CEDD78 CRC64;

Alignment Scores:
 Pred. No.: 163 Length: 190
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.16% Indels: 0
 DB: 12 Gaps: 0

US-09-824-647-16 (1-2095) x Q8QS62 (1-190)

OY 1212 GTGTCGAGCAGCAGCAGCTC 1189
 |||||
 Db 101 ValValArgAlaAlaAspSerLeu 108

RESULT 26

Q9L1T8 PRELIMINARY; PRT; 192 AA.
 ID Q9L1T8
 AC Q9L1T8;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Hypothetical protein SCO2957.
 GN SCO2957 OR SCE59.16C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2) / M145;
 RA Bentley S.D.; Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
 RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT *Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).*;
 RL Nature 417:141-147(2002).
 DR EMBL; AL138851; CAB72203.1;
 KW Hypothetical protein.
 SQ SEQUENCE 192 AA; 19652 MW; C7ACFE12E7BE4B4C CRC64;

Alignment Scores:
 Pred. No.: 163 Length: 192
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.16% Indels: 0
 DB: 16 Gaps: 0

US-09-824-647-16 (1-2095) x Q9L1T8 (1-192)

OY 1088 GCTGTGGTCTGCAGGCTGAGG 1065
 |||||

Tue Jul 8 07:45:17 2003

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Db      156 AlaCysGlySerGlyArgLeuArg 163
RESULT 27
Q9BUX4 PRELIMINARY; PRT; 212 AA.
AC Q9BUX4; 2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 21, Last annotation update)
DE Similar to deoxythymidylate kinase (thymidylate kinase).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MUSCLE;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC001827; AA01827.1; -.
DR HSSP; P00572; 1TMK.
DR InterPro; IPR000062; Thymidylate_kin.
DR Pfam; PF02223; Thymidylate_kin; 1.
DR TIGRFAMs; TIGR00041; DTMK_kinase; 1.
DR PROSITE; PS01331; THYMIDYLATE_KINASE; 1.
KW Kinase.
SQ SEQUENCE 212 AA; 23819 MW; A52876625B3621B1 CRC64;

Alignment Scores:
Pred. No.: 161 Length: 212
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x Q9BUX4 (1-212)
QY 105 GCAGCAGGCCACGACGAGCACTG 82
Db 32 AlaAlaGlyHisArgAlaGluLeu 39

RESULT 28
Q9UQF9 PRELIMINARY; PRT; 214 AA.
AC Q9UQF9; 2001 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 20, Last annotation update)
DE Lysophospholipase isoform.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20499367; PubMed=11042152;
RA Zhang Q.H., Ye M., Wu X.Y., Ren S.X., Zhao M., Zhao C.J., Fu G.,
RA Shen Y., Fan H.Y., Lu G., Zhong M., Xu X.R., Han Z.G., Zhang J.W.,
RA Tao J., Huang Q.H., Zhou J., Hu G.X., Gu J., Chen S.J., Chen Z.;
RT Cloning and functional analysis of cDNAs with open reading frames for
RT 300 previously undefined genes expressed in CD34+ hematopoietic
RT stem/progenitor cells.
RL Genome Res. 10:1546-1560(2000).
RL EMBL; AF077199; AAD26994.1; -.
DR HSSP; Q53547; IAUO.
DR InterPro; IPR003140; PLP_Cesterase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF02230; abhydrolase_2; 1.
SQ SEQUENCE 214 AA; 22875 MW; 63BCC806F509CEB CRC64;

Alignment Scores:
Pred. No.: 161 Length: 214
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x Q9BUX4 (1-212)
QY 105 GCAGCAGGCCACGACGAGCACTG 82
Db 32 AlaAlaGlyHisArgAlaGluLeu 39

RESULT 29
Q9UQF9 PRELIMINARY; PRT; 219 AA.
AC Q9UQF9; 2001 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 20, Last annotation update)
DE Calcium-independent phospholipase A2 isoform 1 (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA MEDLINE=98308497; PubMed=9644627;
RA Portilla D., Crew M.D., Grant D., Serrero G., Bates L.M., Dai G.,
RA Sasser M., Cheng J., Buonanno A.;
RT cDNA cloning and expression of a novel family of enzymes with
RT calcium-independent phospholipase A2 and lysophospholipase
RT activities.
RL J. Am. Soc. Nephrol. 9:1178-1186(1998).
DR EMBL; U97147; AAC63431.1; -.
DR HSSP; Q53547; IAUO.
DR InterPro; IPR003140; PLP_Cesterase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF02230; abhydrolase_2; 1.
DR NON_TER 1
SQ SEQUENCE 219 AA; 23602 MW; 3B6A4FEDC3BC912B CRC64;

Alignment Scores:
Pred. No.: 161 Length: 219
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 6 Gaps: 0

US-09-824-647-16 (1-2095) x Q9UQF9 (1-214)
QY 1686 CTGCTCGCTGCTCGCTCGCTCGCGC 1709
Db 126 LeuSerCysIrpLeuProLeuArg 133

RESULT 30
Q9RRK2 PRELIMINARY; PRT; 229 AA.
AC Q9RRK2; 2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 20, Last annotation update)
DE Cytochrome C4, putative.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/deinococcus group; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1;
RX MEDLINE=20036896; PubMed=10567266;

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RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Yamatchevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans RI.";
RL Science 286:1571-1577(1999).
DR EMBL: AE002078; AAF12028.1; -;
DR HSSP: Q52369; 1ETP.
DR TIGR: DR2487; -;
DR InterPro: IPR00345; CytC_heme_bind.
DR InterPro: IPR003088; Cyt_C1.
DR InterPro: IPR002329; Cyt_C1C.
DR Pfam: PF00034; cytochrome_c; 2.
DR PRINTS: PR00605; CYTOCHROME_C.
DR ProDom: PD004020; Cyt_C1C; 2.
DR PROSITE: PS00190; CYTOCHROME_C; 2.
KW Complete proteome.
SQ SEQUENCE 229 AA; 23957 MW; 23653C80086FCB32 CRC64;

Alignment Scores:
Pred. No.: 160 Length: 229
Score: 8.00 Matches: 8
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 1.15%
Gaps: 0
DB: 16

US-09-824-647-16 (1-2095) x Q9RRK2 (1-229)
QY 1370 GCGGAACCTGCTCCGAGCAGG 1393
DB 133 AlaGluProAlaAlaAlaAlaArg 140

RESULT 31
O75608
ID O75608 PRELIMINARY; PRT; 230 AA.
AC O75608;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Lysophospholipase (Acyl-protein thioesterase-1) (Lysophospholipase
DE 1).
DE DE 1.
GN LPL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hu G.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
SQ SEQUENCE FROM N.A.
RN [2]
RP SEQUENCE FROM N.A.
RA Shen Y., Guan Z., Gu J., Ye M., Zhou J., Zhang Q., Xu S., He K.,
RA Chen S., Mao M., Chen Z.;
RT "Human lysophospholipase gene.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX PubMed=11080636;
RA Davedjiev Y., Dauter Z., Kuznetsov S.R., Jones T.L., Derewenda Z.S.;
RT "Crystal Structure of the Human Acyl Protein Thioesterase I from a
RT Single X-Ray Data Set to 1.5 A.";
RL Structure 8:1137-1146(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE-BONE MARROW;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

[5]
RN SEQUENCE FROM N.A.
RP TISSUE-EYE;
RC Strausberg R.;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF081281; AAC31610.1; -;
DR EMBL: AF077198; AAD26993.1; -;
DR EMBL: AF291053; AAG10063.1; -;
DR EMBL: BC001039; AAH10397.1; -;
DR EMBL: BC008652; AAH08652.1; -;
DR HSSP: Q53547; 1A00.
DR PMMA-2DPAGE; 075608; -;
DR InterPro: IPR003140; PLP_Cesterase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF02230; abhydrolase_2; 1.
SQ SEQUENCE 230 AA; 24669 MW; 90C0522F765F1AC6 CRC64;

Alignment Scores:
Pred. No.: 160 Length: 230
Score: 8.00 Matches: 8
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 1.15%
Gaps: 0
DB: 4

US-09-824-647-16 (1-2095) x O75608 (1-230)
QY 1686 CTGCTCTGCTGGCTTCGCTGCGC 1709
DB 142 LeuSerCysTrpLeuProLeuArg 149

RESULT 32
O77821
ID O77821 PRELIMINARY; PRT; 230 AA.
AC O77821;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Calcium-independent phospholipase A2 isoform 2.
DE Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-KIDNEY;
RA Portilla D., Crew M.D., Grant D., Serrero G., Bates L.M., Dai G.,
RA Sasner M., Cheng J., Buonanno A.;
RT "cDNA cloning and expression of a novel family of enzymes with
RT calcium-independent phospholipase A2 and lysophospholipase
RT activities.";
RL J. Am. Soc. Nephrol. 9:1178-1186(1998).
DR EMBL: U97148; AAC63432.1; -;
DR HSSP: Q53547; 1A00.
DR InterPro: IPR002106; AATRNA_ligaseII.
DR InterPro: IPR003140; PLP_Cesterase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF02230; abhydrolase_2; 1.
DR PROSITE: PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
SQ SEQUENCE 230 AA; 24687 MW; 89AF2017AEFC9FAC CRC64;

Alignment Scores:
Pred. No.: 160 Length: 230
Score: 8.00 Matches: 8
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 1.15%
Gaps: 0
DB: 6

US-09-824-647-16 (1-2095) x O77821 (1-230)
QY 1686 CTGCTCTGCTGGCTTCGCTGCGC 1709

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Db          142 LeuSerCysTrpLeuProLeuArg 149
RESULT 33
P70470
ID P70470 PRELIMINARY; PRT; 230 AA.
AC P70470;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE LYSOPHOSPHOLIPASE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
RC STRAIN-WISTAR; TISSUE=LIVER;
RX MEDLINE=96205961; PubMed=8631810;
RA Sugimoto H., Hayashi H., Yamashita S.;
RT "Purification, cDNA cloning, and regulation of lysophospholipase from
RL rat liver.";
RN J. Biol. Chem. 271:7705-7711(1996).
[2]
SEQUENCE FROM N.A.
RC TISSUE-HYPOTHALAMUS;
RX MEDLINE=98308497; PubMed=9644627;
RA Portilla D., Crew M.D., Grant D., Serrero G., Bates L.M., Dai G.,
RA Sasser M., Cheng J., Buonanno A.;
RT "cDNA cloning and expression of a novel family of enzymes with
RT calcium-independent phospholipase A2 and lysophospholipase
RT activities.";
RL J. Am. Soc. Nephrol. 9:1178-1186(1998).
DR EMBL; D63885; BAA09935.1; -
DR EMBL; U97146; AAC63430.1; -
DR HSSP; Q53547; LAUO.
DR InterPro; IPR002106; RAIRNA_ligaseII.
DR InterPro; IPR003140; PLP_Cesterase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF02230; abhydrolase_2; 1.
DR PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
SQ SEQUENCE 230 AA; 24709 MW; AAF8C4702EAAD74 CRC64;

Alignment Scores:
Pred. No.: 160 Length: 230
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 11 Gaps: 0

US-09-824-647-16 (1-2095) x P70470 (1-230)
QY 1686 CTGCTCGCTGCTGCTGCTGCTGCGC 1709
Db 142 LeuSerCysTrpLeuProLeuArg 149
RESULT 34
P97823
ID P97823 PRELIMINARY; PRT; 230 AA.
AC P97823;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE LPHOSPHOLIPASE 1A (EC 3.1.1.5) (Lysophospholipase I) (LBCITHINASE B)
DE (LYSOLECITHINASE) (Phospholipase B) (Adult MALE kidney CDNA, RIKEN
DE FULL-length enriched LIBRARY, clone:0610025N20, FULL INSERT sequence)
DE (Lysophospholipase I).
GN LYPLAL OR PLAL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN SEQUENCE FROM N.A.
RP Wang A., Deems R.A., Dennis E.A.;
RL J. Biol. Chem. 0:0-0(0).
[2]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Imanaka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kusakawa T., Saito K.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Havaehizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN Nature 409:685-690(2001).
[3]
SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2-LYSOPHOSPHATIDYLCHOLINE + H(2)O -
CC GLYCEROPHOSPHOCHOLINE + A FATTY ACID ANION.
DR EMBL; U89352; AAB48627.1; -
DR EMBL; AK002674; BAB22276.1; -
DR EMBL; BC013536; AAHL3536.1; -
DR HSSP; Q53547; LAUO
DR MGD; MGI:1344588; Lyplal.
DR InterPro; IPR002106; AATRNA_ligaseII.
DR InterPro; IPR003140; PLP_Cesterase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF02230; abhydrolase_2; 1.
DR PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
RW Hydrolase.
SQ SEQUENCE 230 AA; 24687 MW; 89AF2017AEFC9FAC CRC64;

Alignment Scores:
Pred. No.: 160 Length: 230
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 11 Gaps: 0

US-09-824-647-16 (1-2095) x P97823 (1-230)
QY 1686 CTGCTCGCTGCTGCTGCTGCTGCGC 1709
Db 142 LeuSerCysTrpLeuProLeuArg 149
RESULT 35
Q9V8A8
ID Q9V8A8 PRELIMINARY; PRT; 253 AA.
AC Q9V8A8;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE CG5767 protein.
DE CG5767.
GN Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

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OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.J., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Barker E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Abrell J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fouts D.C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glöckle A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhu S., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 DR EMBL; AF003801; AAF57763.1;
 DR FlyBase; FBgn0034292; CG5767.
 SQ SEQUENCE 253 AA; 25956 MW; 22A35668145C1946 CRC64;

Alignment Scores:
 Pred. No.: 158 Length: 253
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.15% Indels: 0
 DB: 5 Gaps: 0

US-09-824-647-16 (1-2095) x Q9V8A8 (1-253)
 QY 1208 ACCACGACGACGTCGCCCGAGC 1231
 Db 191 ThrThrSerThrAlaAlaProSer 198
 RESULT 36
 Q9RZ01
 ID Q9RZ01 PRELIMINARY; PRT: 253 AA.
 AC Q9RZ01;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2002 (TREMBLrel. 20, Last annotation update)
 DE Transcriptional regulator, ICLR family.
 GN DRA0152.
 OS Deinococcus radiodurans.

OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
 OC Deinococcaceae; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R1;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1."
 RL Science 286:1571-1577(1999).
 CC -1- SIMILARITY: BELONGS TO THE ICLR FAMILY OF TRANSCRIPTIONAL REGULATORS.
 CC EMBL; AE001862; AAF12212.1;
 DR TIGR; DRA01521.1;
 DR InterPro; IPR000285; HTH_ICLR.
 DR Pfam; PF01614; ICLR; 1.
 DR SMART; SM00346; HTH_ICLR; 1.
 KW DNA-binding; Transcription regulation; Complete proteome.
 SQ SEQUENCE 253 AA; 27299 MW; DBB8F05ABE6F65A8 CRC64;

Alignment Scores:
 Pred. No.: 158 Length: 253
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.16% Indels: 0
 DB: 16 Gaps: 0

US-09-824-647-16 (1-2095) x Q9RZ01 (1-253)
 QY 290 CGCATGCGACGCGCTCTGGGAAG 267
 Db 135 ProHisAlaThrAlaSerGlyLys 142
 RESULT 37
 Q9ATL6
 ID Q9ATL6 PRELIMINARY; PRT: 255 AA.
 AC Q9ATL6;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Tonoplast membrane integral protein zmfTIP4-1.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21140306; PubMed=11244102;
 RA Chaumont F., Barrieu F., Wojcik E., Chrispeels M.J., Jung R.;
 RT "Aquaporins constitute a large and highly divergent protein family in maize."
 RL Plant Physiol. 125:1206-1215(2001).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).
 DR EMBL; AF326505; AAK26772.1;
 DR HSP; P29972; IFQY.
 DR InterPro; IPR000425; MIP_family.
 DR Pfam; PF00230; MIP; 1.
 DR PRINTS; PD00783; MINTRINSCP.
 DR ProDom; PD000295; MIP_family; 1.
 DR PROSITE; PS00221; MIP; 1.
 KW Transmembrane; Transport.
 SQ SEQUENCE 255 AA; 26519 MW; DDD4C1AC3E7DB8D1 CRC64;

遊

ID	O69819	PRELIMINARY;	PRT;	256 AA.
AC	O69819;			
DT	01-AUG-1998	(TREMBLrel. 07, Created)		
DT	01-AUG-1998	(TREMBLrel. 07, Last sequence update)		
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)		
DE	Hypothetical protein SCO6425.			
GN	SCO6425 OR SC1A6.14.			
OS	Streptomyces coelicolor.			
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;			
OC	Actinomycetales; Streptomycineae; Streptomycetaceae; Str			
OX	NCBI_TaxID=1902;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-A3(2);			
RA	Oliver K., Harris D.;			
RL	Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.			

CC -1- SIMILARITY: BELONGS TO THE ARAC/XLYS FAMILY OF TRANSCRIPTIONAL REGULATORS.

CC
CC
REGULATORS.

DR EMBL; AL023496; CAA18912.1; -

DR InterPro; IPR000005; HTHArAc.

DR Pfam; PF00165; HTH_AraC; 2.

DR . PRINTS; PR00032; HTHARAC.

DR SMART; SM00342; HTH_ARAC; 1.

DR PROSITE; PS00041; HTH_ARAC_FA

DR PROSITE; PS01124; HTH_ARAC_FAM1

DNA-binding; Hypothetical protein

SQ SEQUENCE 256 AA; 27/61 MW;

1000

Alignment scores: 150

Pred. No.:	138
Score:	9 00

00:00:21:035

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.15% Indels: 0
 DB: 16 Gaps: 0

US-09-824-647-16 (1-2095) x 069819 (1-256)

QY 308 GCCACGCGGCTCCACTGAGTG 331
 Db 48 AlahisGlyAlaserThrAlaval 55

RESULT 40

O68521
 ID O68521 PRELIMINARY; PRT; 257 AA.
 AC O68521; 1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical 28.6 kDa protein.
 OS Myxococcus xanthus
 OC Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
 OC Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
 OX NCBI_TaxID=34;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-DZF1;
 RX MEDLINE-96347136; PubMed-8736543;
 RA Trudeau K.G., Ward M.J., Zusman D.R.;
 RT "Identification and characterization of Frzz, a novel response
 RT regulator necessary for swarming and fruiting-body formation in
 RT Myxococcus xanthus";
 RL Mol. Microbiol. 20:645-655(1996).
 RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-DZF1;
 RX MEDLINE-99009001; PubMed-9791117;
 RA Ward M.J., Lew H., Treuner-Lange A., Zusman D.R.;
 RT "Regulation of motility behavior in Myxococcus xanthus may require an
 RT extracytoplasmic-function sigma factor";
 RL J. Bacteriol. 180:5668-5675(1998).
 DR EMBL; AF049107; AAC98489.1;
 KW Hypothetical protein.
 SQ SEQUENCE 257 AA; 28575 MW; 860E35015266C7EB CRC64;

Alignment Scores:
 Pred. No.: 158 Length: 257
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.15% Indels: 0
 DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x 068521 (1-257)

QY 1187 CAGAGCTGCTGCTCGGACC 1210
 Db 66 GlnargLeuserAlaAlaArgThr 73

RESULT 41

Q9ATL5
 ID Q9ATL5 PRELIMINARY; PRT; 257 AA.
 AC Q9ATL5; 2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Tonoplast membrane integral protein ZmTIP4-2.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE-21140306; PubMed-11244102;
 RA Chaumont F., Barrieu F., Wojcik E., Chrispeels M.J., Jung R.;
 RT "Aquaporins constitute a large and highly divergent protein family in
 RT maize";
 RL Plant Physiol. 125:1206-1215(2001).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).
 DR EMBL; AF326506; AAK26773.1;
 DR HSP; P29972; IFOY.
 DR InterPro; IPR000425; MIP_family.
 DR Pfam; PF00230; MIP; 1.
 DR PRINTS; PR00783; MINTINSICP.
 DR ProDom; PD000295; MIP_family; 1.
 DR PROSITE; PS00221; MIP; 1.
 KW Transmembrane; Transport.
 SQ SEQUENCE 257 AA; 26603 MW; 465414DFCB7F7BE9 CRC64;

Alignment Scores:
 Pred. No.: 158 Length: 257
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.16% Indels: 0
 DB: 10 Gaps: 0

US-09-824-647-16 (1-2095) x 09ATL5 (1-257)

QY 1362 GCAGCTGCTGCTGCACGCC 1339
 Db 74 AlaAlaGlyValLeuValThrAla 81

RESULT 42

Q39263
 ID Q39263 PRELIMINARY; PRT; 259 AA.
 AC Q39263;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Zinc finger protein.
 GN ZFP4.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LANDSBERG ERECTA; TISSUE=ROOT;
 RX MEDLINE-95322589; PubMed-7599312;
 RA Tsuge B.W., Goodman H.M.;
 RT "Characterization of a family of Arabidopsis zinc finger protein
 RT cDNAs";
 RL Plant Mol. Biol. 28:267-279(1995).
 DR EMBL; L39647; AAA87300.1;
 DR TRANSFAC; T03965;
 DR InterPro; IPR000822; znf_C2H2.
 DR Pfam; PF00096; zf_C2H2; 1.
 DR SMART; SM00355; znf_C2H2; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1;
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.
 KW DNA-binding; Metal-binding; zinc-finger.
 SQ SEQUENCE 259 AA; 28644 MW; AE8F1B4A280067FD CRC64;

Alignment Scores:
 Pred. No.: 158 Length: 259
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.16% Indels: 0
 DB: 10 Gaps: 0

US-09-824-647-16 (1-2095) x Q39263 (1-259)

OY 1269 TCCTCGCTGACACTGCCCTCAGC 1246
 Db 55 SerSerLeuthrLeupProLeuSer 62
 RESULT 43
 Q9C8D2 PRELIMINARY; PRT; 260 AA.
 AC Q9C8D2; 2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE C2H2-type zinc finger protein, putative (At1g66140/F15E12_19).
 GN F15E12_19.
 GN Arabidopsis thaliana (Mouse-ear cress).
 OS Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
 Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Dewar K.,
 Chung M.K., Conn L., Conway A.B., Conway T.H., Creasy T.H., Dewar K.,
 Dunn P., Etgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
 Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kvan A., Lam B.,
 Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
 Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 Suo H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 Uterback T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,
 Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 thaliana.";
 RL Nature 408:816-820(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Banh J., Bowser L.,
 Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y., Ishida J.,
 Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M.,
 Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M., Seki M.,
 Southwick A., Toriumi M., Yamada K., Yu G., Shinzaki K., Davis R.W.,
 Theologis A., Ecker J.R.;
 RA "Arabidopsis cDNA clones.";
 RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
 Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A.,
 Ecker J.R.;
 RA "Arabidopsis cDNA clones.";
 RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Koesema E., Chen H., Cheuk R., Kim C.J., Meyers M.C., Shinn P.,
 Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
 Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
 Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
 Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
 Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,

RA Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;
 RT "Arabidopsis ORF clones.";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC026480; AAG51296.1; -
 DR EMBL; AF361630; AAK32798.1; -
 DR EMBL; AY058087; AAL24195.1; -
 DR EMBL; AY058067; AAL06967.1; -
 DR InterPro: IPR000822; Znf.C2H2.
 DR Pfam: PF00096; Znf.C2H2; 1.
 DR SMART: SM00355; Znf.C2H2; 1.
 DR PROSITE; PS0028; ZINC_FINGER_C2H2_1; 1.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.
 KW DNA-binding; Metal-binding; Zinc-finger.
 SQ SEQUENCE 260 AA; 28308 MW; 48484EC120250F09 CRC64;
 Alignment Scores:
 Pred. No.: 158 Length: 260
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.16% Indels: 0
 DB: 10 Gaps: 0
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 OY 1269 TCCTCGCTGACACTGCCCTCAGC 1246
 Db 55 SerSerLeuthrLeupProLeuSer 62
 RESULT 44
 Q8RUU4 PRELIMINARY; PRT; 260 AA.
 ID Q8RUU4
 AC Q8RUU4; 2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE OSJNBA0026J14.33 protein (OSJNBA0042P21.8 protein).
 DE OSJNBA0026J14.33 OR OSJNBA0042P21.8
 GN OSJNBA0026J14.33 OR OSJNBA0042P21.8
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RA "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
 clone:OSJNBA0026J14.";
 RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RA "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
 clone:OSJNBA0042P21.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP004231; BAB89246.1; -
 DR EMBL; AP004614; BAB90800.1; -
 SQ SEQUENCE 260 AA; 26845 MW; 7C73972A6ECA4BEF CRC64;
 Alignment Scores:
 Pred. No.: 158 Length: 260
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.16% Indels: 0
 DB: 10 Gaps: 0
 US-09-824-647-16 (1-2095) x Q8RUU4 (1-260)
 OY 1219 AGTGTGCTGGTCCGAGCAGCAGA 1196
 Db 55 SerSerLeuthrLeupProLeuSer 62

Db 115 SerAlaGlyProSerSerArg 122

RESULT 45

Q99MA1 PRELIMINARY; PRU; 269 AA.

AC Q99MA1

DT 01-JUN-2001 (TRENBLrel. 17, Created)

DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)

DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)

DE Transcription factor MRG1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID-10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-SPRAGUE-DAWLEY;

RA Zhuang D.Z., Chou Y.-T., Yang Y.-C.;

RT "Structural and functional conservation of MRG family in system evolution";

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF361476; AAK30621.1; -

SQ SEQUENCE 269 AA; 28291 MW; 038DC4B21E4E21F1 CRC64;

Alignment Scores:

Pred. No.:	157	Length:	269
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.16%	Indels:	0
DB:	11	Gaps:	0

US-09-824-647-16 (1-2095) x Q99MA1 (1-269)

QY 1231 GCTGGGGCAGCAGTGTGTGGT 1208

DB 186 ALAGLYGlySerAlaGlyGly 193

Search completed: July 7, 2003, 16:00:37

Job time : 186.5 secs

GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: July 7, 2003, 16:00:43 ; Search time 29 Seconds
(without alignments)
4251.105 Million cell updates/sec

Title: US-09-824-647-16

Perfect score: 694

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Fgapop 6.0 , Fgapext 7.0
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Searched: 262574 seqs, 29422922 residues

Word size: 1

Total number of hits satisfying chosen parameters: 136828

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Listing first 45 summaries

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-LOOPEXT=0 -UNITS-bits -START=1 -END=1 -MATRIX-oligo -TRANS-human40.cdi
-LIST=45 -DOALIGN=200 -THRSCORE-quality -THR_MIN=1 -ALIGN=45 -MODE-LOCAL
-OUTFWT-pto -NORM-ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=15
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-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued_Patents_AA.*

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6: /cgn2_6/ptodata/1/1aa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	2.0	14	4	US-08-991-862-7
2	11	1.6	15	1	US-08-245-853-2
3	11	1.6	15	1	US-08-573-675-2
4	11	1.6	15	6	5470825-2
5	7	1.0	14	4	US-08-991-862-5
6	6	0.9	8	4	US-08-419-826-39
7	6	0.9	9	2	US-08-244-951A-7
8	6	0.9	9	2	US-08-389-011-5
9	6	0.9	9	2	US-08-934-222-113
10	6	0.9	9	2	US-08-933-402-113
11	6	0.9	9	2	US-09-207-621-113
12	6	0.9	9	2	US-08-532-818-113

c 13	6	0.9	9	3	US-08-403-917A-5	Sequence 5, Appli
14	6	0.9	9	3	US-09-231-797-113	Sequence 113, App
15	6	0.9	9	3	US-08-934-224-113	Sequence 113, App
16	6	0.9	9	3	US-08-933-843-113	Sequence 113, App
17	6	0.9	9	4	US-08-934-223-113	Sequence 113, App
c 18	6	0.9	9	4	US-09-348-952A-5	Sequence 5, Appli
19	6	0.9	9	4	US-09-413-492-113	Sequence 113, App
20	6	0.9	9	4	US-09-053-611-6	Sequence 6, Appli
21	6	0.9	9	6	5470825-3	Patent No. 5470825
22	6	0.9	10	4	US-08-847-844A-80	Sequence 80, Appli
23	6	0.9	10	4	US-09-220-528-91	Sequence 91, Appli
c 24	6	0.9	10	4	US-09-099-543C-27	Sequence 27, Appli
25	6	0.9	11	4	US-09-461-691-66	Sequence 66, Appli
c 26	6	0.9	12	4	US-08-672-850-19	Sequence 19, Appli
27	6	0.9	13	2	US-08-726-306A-161	Sequence 161, App
c 28	6	0.9	13	4	US-08-602-999A-82	Sequence 82, Appli
c 29	6	0.9	13	4	US-08-278-868-82	Sequence 82, Appli
30	6	0.9	13	4	US-09-183-841-4	Sequence 4, Appli
c 31	6	0.9	13	4	US-09-500-124-82	Sequence 82, Appli
32	6	0.9	13	4	US-08-766-596A-40	Sequence 40, Appli
c 33	6	0.9	14	1	US-08-445-745-120	Sequence 120, App
34	6	0.9	14	3	US-09-120-365-82	Sequence 82, Appli
35	6	0.9	14	3	US-09-120-365-83	Sequence 83, Appli
36	6	0.9	14	3	US-09-120-365-84	Sequence 84, Appli
37	6	0.9	14	3	US-09-515-039-82	Sequence 86, Appli
38	6	0.9	14	4	US-09-515-039-83	Sequence 83, Appli
39	6	0.9	14	4	US-09-515-039-84	Sequence 84, Appli
40	6	0.9	14	4	US-09-515-039-86	Sequence 86, Appli
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c 42	6	0.9	14	4	US-09-302-305C-4	Sequence 4, Appli
43	6	0.9	14	4	US-09-302-305C-17	Sequence 17, Appli
44	6	0.9	14	4	US-09-248-061B-9	Sequence 9, Appli
c 45	6	0.9	14	4		

ALIGNMENTS

RESULT 1

US-08-991-862-7
; Sequence 7, Application US/08991862
; Patent No. 6309826
; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996.488/P001-A
; CURRENT APPLICATION NUMBER: US/08/991,862
; CURRENT FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/863,862
; EARLIER FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Human granulin
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(14)
; OTHER INFORMATION: Internal peptide of human GP88 used to develop
; OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody.
US-08-991-862-7

Alignment Scores:

Align No.:	0-000321	Length:	14
Score:	14.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	4	Gaps:	0

US-09-824-647-16 (1-2095) x US-08-991-862-7 (1-14)

QY 1708 GCACGCGGGGTACCAAGTGTTCGCGAGGAGGCCGCGC 1749

QY 865 GACATGGAGTGCAGTCCACATGGCTATACC 897
Db 5 AspMetGluValSerCysProAspGlyTyrThr 15
|||||

RESULT 5

US-08-991-862-5
; Sequence 5, Application US/08991862
; Patent No. 6309826
; GENERAL INFORMATION:
; APPLICANT: Seirero, Gnette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: Z9996.488/P001-A
; CURRENT APPLICATION NUMBER: US/08/991,862
; CURRENT FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/863,862
; EARLIER FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: mouse granuln
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(14)
; OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the
; OTHER INFORMATION: antisera against the GP88 used in the
; OTHER INFORMATION: immunoaffinity step.
US-08-991-862-5

Alignment Scores:
Pred. No.: 640 Length: 14
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.01% Indels: 0
DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x US-08-991-862-5 (1-14)

QY 1714 AGGGTACCAAGTGTTCGC 1734
Db 3 ArgGlyThrLysCysLeuArg 9
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RESULT 6

US-09-419-826-39
; Sequence 39, Application US/09419826
; Patent No. 6306832
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDE ANTIESTROGEN COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR TREATING BREAST CANCER
; NUMBER OF SEQUENCES: 39
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/419,826
; FILING DATE: 14-OCT-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/07711
; FILING DATE: 14-APR-1998
; APPLICATION NUMBER: US 60/043,545
; FILING DATE: 14-APR-1997
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear

US-09-419-826-39

Alignment Scores:
Pred. No.: 7,23e+06 Length: 8
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-419-826-39 (1-8)

QY 1131 CTCCTCCGATACCTGCTG 1148
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RESULT 7

US-08-244-951A-7
; Sequence 7, Application US/08244951A
; Patent No. 5843779
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VANMECHELEN, EUGEN; VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: DIRECTED AGAINST THE MICROFIBULE-ASSOCIATED
; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMA SECRETING THESE
; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03499
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403403.6
; FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410,003A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown

US-08-244-951A-7

Alignment Scores:
Pred. No.: 6,43e+06 Length: 9
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.87% Indels: 0
DB: 2 Gaps: 0

us-09-824-647-16.1m.rai

Tue Jul 8 07:45:07 2003

US-09-824-647-16 (1-2095) x US-08-389-011-5 (1-9)

QY 465 GGGCAGCAGCCCGCAGGA 448
 DB 1 GlyAlaAlaProGly 6

RESULT 8

US-08-389-011-5
 ; Sequence 5, Application US/08389011
 ; Patent No. 5961257

GENERAL INFORMATION:
 APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
 APPLICANT: VANDERMEEREN, EUGEN; VAN DE VOORDE, ANDRE
 TITLE OF INVENTION: MONOCLONAL ANTIBODIES
 TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
 TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
 TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
 TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS.
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIERMAN & MUSERLIAN
 STREET: 600 THIRD AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10016

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/389,011
 FILING DATE: 15-FEB-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/403,917
 FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/403,916
 FILING DATE: 19-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/244,951
 FILING DATE: 13-JUN-1994

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP93/03499
 FILING DATE: 10-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP/92/403403.6
 FILING DATE: 14-DEC-1992

ATTORNEY/AGENT INFORMATION:
 NAME: CHARLES A. MUSERLIAN
 REGISTRATION NUMBER: 19,683
 REFERENCE/DOCKET NUMBER: 410.003-1-CON
 TELEPHONE: (212) 661-8000
 TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 5:
 LENGTH: 9
 TYPE: Amino Acid
 STRANDEDNESS: Unknown
 TOPOLOGY: Unknown

US-08-389-011-5

Alignment Scores:
 Pred. No.: 6.43e+06
 Score: 6.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 0.87%
 DB: 2

Length: 9
 Matches: 6
 Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-08-934-222-113

QY 465 GGGCAGCAGCCCGCAGGA 448
 DB 1 GlyAlaAlaProGly 6

RESULT 9

US-08-934-222-113
 ; Sequence 113, Application US/08934222
 ; Patent No. 5928896
 ; GENERAL INFORMATION:

APPLICANT: EVANS, Herbert J.
 APPLICANT: KANI, R. Manjunatha
 TITLE OF INVENTION: Polypeptides That Include Conformation-
 TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interact-
 TITLE OF INVENTION: Site
 NUMBER OF SEQUENCES: 153
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: Suite 500, 3000 K Street NW
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20007

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/934,222
 FILING DATE: 19-SEPT-1997

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/532,818
 FILING DATE: 03-MAY-1996

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: U.S. 08/143,364
 FILING DATE: 29-OCT-1993

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: U.S. 08/051,741
 FILING DATE: 23-APR-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Isacson, John P.
 REGISTRATION NUMBER: 33,751
 REFERENCE/DOCKET NUMBER: 040433/0148

INFORMATION FOR SEQ ID NO: 113:
 LENGTH: 9 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

US-08-934-222-113

Alignment Scores:
 Pred. No.: 6.43e+06
 Score: 6.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 0.86%
 DB: 2

Length: 9
 Matches: 6
 Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-09-824-647-16 (1-2095) x US-08-934-222-113 (1-9)

QY 270 CCCAGAGCCGTCGTCATG 287
 DB 1 ProArgGlyArgGlyMet 6

RESULT 10

US-08-933-402-113
 ; Sequence 113, Application US/08933402
 ; Patent No. 5948887
 ; GENERAL INFORMATION:
 ; APPLICANT: EVANS, Herbert J.

APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
CONSTRAINING GROUPS WHICH FLANK A PROTEIN-PROTEIN INTERACTION
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,402
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
PRIORITY DATE: 03-MAY-1996
PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-933-402-113
Alignment Scores:
Pred. No.: 6.43e+06 Length: 9
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 2 Gaps: 0
US-09-824-647-16 (1-2095) x US-08-933-402-113 (1-9)
QY 270 CCCAGAGCGGTGGCATG 287
DB 1 ProArgGlyArgGlyMet 6
RESULT 11
US-09-207-621-113
Sequence 113, Application US/09207621
Patent No. 5952465
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
CONSTRAINING GROUPS WHICH FLANK A PROTEIN-PROTEIN INTERACTION
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/207,621
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
PRIORITY DATE: 03-MAY-1996
PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-207-621-113
Alignment Scores:
Pred. No.: 6.43e+06 Length: 9
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 2 Gaps: 0
US-09-824-647-16 (1-2095) x US-09-207-621-113 (1-9)
QY 270 CCCAGAGCGGTGGCATG 287
DB 1 ProArgGlyArgGlyMet 6
RESULT 12
US-08-532-818-113
Sequence 113, Application US/08532818
Patent No. 5965698
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
CONSTRAINING GROUPS WHICH FLANK A PROTEIN-PROTEIN INTERACTION
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364

us-09-824-647-16.lim.ra

Tue Jul 8 07:45:07 2003

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; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-532-818-113

Alignment Scores:
Pred. No.: 6.43e+06 Length: 9
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x US-08-532-818-113 (1-9)
QY 270 CCCAGAGCCGTGGCATG 287
Db 1 Proargglyargglymet 6

RESULT 13
US-08-403-917A-5
; Sequence 5, Application US/08403917A
; Patent No. 6010913
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VANDEVOORDE, EUGEN;
; APPLICANT: VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERNAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,917A
; FILING DATE: 19-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,167
; FILING DATE: 27-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/244,951
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03499
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403403.6
; FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683

; REFERENCE/DOCKET NUMBER: 410.003-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
US-08-403-917A-5

Alignment Scores:
Pred. No.: 6.43e+06 Length: 9
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.87% Indels: 0
DB: 3 Gaps: 0

US-09-824-647-16 (1-2095) x US-08-403-917A-5 (1-9)
QY 465 GGGCAGCACCCACGGA 448
Db 1 GlyAlaAlaProGly 6

RESULT 14
US-09-231-797-113
; Sequence 113, Application US/09231797
; Patent No. 6084066
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides that include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interacti
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/231,797
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-231-797-113
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Alignment Scores:
Pred. No.: 6.43e+06 Length: 9
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 3 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-231-797-113 (1-9)

QY 270 CCAGAGCGCGTGGCATG 287
Db 1 ProArgGlyArgGlyMet 6

RESULT 15

US-08-934-224-113
; Sequence 113, Application US/08934224
; Patent No. 6100044

GENERAL INFORMATION:

APPLICANT: EVANS, Herbert J.

APPLICANT: KINI, R. Manjunatha

TITLE OF INVENTION: Polypeptides That Include Conformation-

TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction

TITLE OF INVENTION: Site

NUMBER OF SEQUENCES: 153

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: Suite 500, 3000 K Street NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/934,224

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/532,818

FILING DATE: 03-MAY-1996

APPLICATION NUMBER: PCT/US94/04294

FILING DATE: 21-APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/143,364

FILING DATE: 29-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/051,741

FILING DATE: 23-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Isaacson, John P.

REGISTRATION NUMBER: 33,751

REFERENCE/DOCKET NUMBER: 040433/0148

INFORMATION FOR SEQ ID NO: 113:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-934-224-113

Alignment Scores:

Pred. No.: 6.43e+06 Length: 9
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 3 Gaps: 0

US-09-824-647-16 (1-2095) x US-08-934-224-113 (1-9)

QY 270 CCAGAGCGCGTGGCATG 287

Db 1 ProArgGlyArgGlyMet 6

RESULT 16

US-08-933-843-113

; Sequence 113, Application US/08933843

; Patent No. 6111069

; GENERAL INFORMATION:

APPLICANT: EVANS, Herbert J.

APPLICANT: KINI, R. Manjunatha

TITLE OF INVENTION: Polypeptides That Include Conformation-

TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Inter

TITLE OF INVENTION: Site

NUMBER OF SEQUENCES: 153

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: Suite 500, 3000 K Street NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/933,843

FILING DATE: 19-SEPT-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/532,818

FILING DATE: 03-MAY-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/143,364

FILING DATE: 29-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/051,741

FILING DATE: 23-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Isaacson, John P.

REGISTRATION/DOCKET NUMBER: 33,751

REFERENCE/DOCKET NUMBER: 040433/0148

INFORMATION FOR SEQ ID NO: 113:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-933-843-113

Alignment Scores:

Pred. No.: 6.43e+06 Length: 9
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 3 Gaps: 0

US-09-824-647-16 (1-2095) x US-08-933-843-113 (1-9)

QY 270 CCAGAGCGCGTGGCATG 287

Db 1 ProArgGlyArgGlyMet 6

RESULT 17

US-08-934-223-113

; Sequence 113, Application US/08934223

; Patent No. 6147189

; GENERAL INFORMATION:

APPLICANT: EVANS, Herbert J.

APPLICANT: KINI, R. Manjunatha

TITLE OF INVENTION: Polypeptides That Include Conformation-

TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Intera

TITLE OF INVENTION: Site

us-09-824-647-16.lim.ra1

Tue Jul 8 07:45:07 2003

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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/348,952A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,917
FILING DATE: 19-JAN-1995
APPLICATION NUMBER: 08/256,167
FILING DATE: 27-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
APPLICATION DATA: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410,003-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
US-09-348-952A-5

Alignment Scores:
Pred. No.: 6.43e+06
Score: 6.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0.87%
Indels: 4
Gaps: 0
DB: 0

US-09-824-647-16 (1-2095) x US-09-348-952A-5 (1-9)

QY 465 GGGCAGCAGCCCCAGGA 448
Db 1 GlyAlaAlaProGly 6

RESULT 19
US-09-413-492-113
Sequence 113, Application US/09413492
Patent No. 6258550
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
That Flank A Protein-Protein Interac
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interac
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,223
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA: U.S. 08/051,741
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-934-223-113

Alignment Scores:
Pred. No.: 6.43e+06
Score: 6.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0.86%
Indels: 4
Gaps: 0
DB: 0

US-09-824-647-16 (1-2095) x US-08-934-223-113 (1-9)

QY 270 CCCAGAGCCGTGGCATG 287
Db 1 ProArgGlyArgGlyMet 6

RESULT 18
US-09-348-952A-5
Sequence 5, Application US/09348952A
Patent No. 6232437
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANMECHELEN, EUGEN;
APPLICANT: VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016

```

```

NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,223
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA: U.S. 08/051,741
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-934-223-113

Alignment Scores:
Pred. No.: 6.43e+06
Score: 6.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0.86%
Indels: 4
Gaps: 0
DB: 0

US-09-824-647-16 (1-2095) x US-08-934-223-113 (1-9)

QY 270 CCCAGAGCCGTGGCATG 287
Db 1 ProArgGlyArgGlyMet 6

RESULT 18
US-09-348-952A-5
Sequence 5, Application US/09348952A
Patent No. 6232437
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANMECHELEN, EUGEN;
APPLICANT: VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016

```

SOFTWARE: PatentIn Release #1.0, Version #1.25

APPLICATION NUMBER: US/09/413,492

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/532,818

FILING DATE: 03-MAY-1996

APPLICATION NUMBER: PCT/US94/04294

FILING DATE: 21-APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/143,364

FILING DATE: 29-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/051,741

FILING DATE: 23-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Isaacson, John P.

REGISTRATION NUMBER: 33,751

REFERENCE/DOCKET NUMBER: 040433/0148

INFORMATION FOR SEQ ID NO: 113:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-09-413-492-113

Alignment Scores:

Pred. No.: 9 Length: 6.43e+06
Score: 6.00 Matches: 9
Percent Similarity: 100.00% Conservative: 6
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-413-492-113 (1-9)

QY 270 CCCAGAGCGGTGCATG 287

Db 1 ProArgGlyArgGlyMet 6

RESULT 20

US-09-053-611-6

Sequence 6, Application US/09053611

Patent No. 6410245

GENERAL INFORMATION:

APPLICANT: No. 6410245throp, Jeffrey P.

APPLICANT: Hart, Charles P.

APPLICANT: Schatz, Peter J.

APPLICANT: Glaxo Group Limited

TITLE OF INVENTION: Compositions and Methods for Detecting Ligand Dependent

FILE REFERENCE: 2064

CURRENT FILING DATE: 1998-04-01

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 6

LENGTH: 9

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:LCD (leucine

OTHER INFORMATION: charged domain)

US-09-053-611-6

Alignment Scores:

Pred. No.: 9 Length: 6.43e+06
Score: 6.00 Matches: 9
Percent Similarity: 100.00% Conservative: 6
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-053-611-6 (1-9)

QY 1131 CTCCTCCGATACCTGCTG 1148

Db 1 LeuLeuArgTyrLeuLeu 6

RESULT 21

5470825-3

Patent No. 5470825

APPLICANT: SCOTT, RANDY W.;GLEICH, GERALD J.;

WILDE, CRAIG G.

TITLE OF INVENTION: BASOPHIL GRANULE PROTEINS

NUMBER OF SEQUENCES: 8

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/259,564

FILING DATE: 15-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 551,263

FILING DATE: 10-JUL-1990

SEQ ID NO:3:

LENGTH: 9

5470825-3

Alignment Scores:

Pred. No.: 9 Length: 6.43e+06
Score: 6.00 Matches: 9
Percent Similarity: 100.00% Conservative: 6
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 6 Gaps: 0

US-09-824-647-16 (1-2095) x 5470825-3 (1-9)

QY 637 CCGAGCGACGTCGCGG 654

Db 1 ProAspAlaArgSerArg 6

RESULT 22

US-08-847-844A-80

Sequence 80, Application US/08847844A

Patent No. 6150160

GENERAL INFORMATION:

APPLICANT: KAZAZIAN JR., HAIG H.

APPLICANT: BOEKE, JEFF D.

APPLICANT: MORAN, JOHN V.

APPLICANT: DOMBROSKI, BETH A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF

TITLE OF INVENTION: MAMMALIAN RETROTRANSPOSONS

NUMBER OF SEQUENCES: 137

CORRESPONDENCE ADDRESS:

ADDRESSER: PANITCH SCHWARZE JACOBS & NADEL, P.C.

STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND FL.

CITY: PHILADELPHIA

STATE: PA

COUNTRY: U.S.A.

ZIP: 19103-7086

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/847,844A

FILING DATE: 28-APR-1997

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/749,805

FILING DATE: 16-NOV-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/006,831

FILING DATE: 16-NOV-1995

ATTORNEY/AGENT INFORMATION:

NAME: DOYLE LEARY Ph.D., KATHRYN

us-09-824-647-16.lim.ra

Tue Jul 8 07:45:07 2003

APPLICANT: Cerottini, Jean-Charles
APPLICANT: Romero, Pedro
TITLE OF INVENTION: Isolated No. 6326200a - And Decapeptides Which Bind
TO HLA Molecules, and the Use Thereof
FILE REFERENCE: LUD 5483.2
CURRENT APPLICATION NUMBER: US/09/099,543C
CURRENT FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: US 09/061,388
PRIOR FILING DATE: 1998-04-16
PRIOR APPLICATION NUMBER: US 08/880,963
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 27
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Derivative of SEQ ID NO:1
US-09-099-543C-27
Alignment Scores:
Pred. No.: 5.37e+03
Score: 6.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0.87%
Indels: 0
Gaps: 0
DB:
US-09-824-647-16 (1-2095) x US-09-099-543C-27 (1-10)

QY 903 GCAGCAGGTATAGCCATC 886
DB 2 AlaAlaGlyLeuAlaLeu 7

RESULT 25
US-09-461-697-66
Sequence 66, Application US/09461697
Patent No. 6277974
GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: LO, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Katz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 66
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-09-461-697-66

Alignment Scores:
Pred. No.: 5.28e+03
Score: 6.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0.87%
Indels: 0
Gaps: 0
DB:
US-09-824-647-16 (1-2095) x US-09-461-697-66 (1-11)

QY 1311 GCGGCGGCGAGCATCTT 1294
DB 3 AlaAlaGlyArgHisLeu 8

REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 9596-2302
TELEPHONE: 215-567-2020
TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-847-844A-80
Alignment Scores:
Pred. No.: 5.37e+03
Score: 6.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0.86%
Indels: 0
Gaps: 0
DB:
US-09-824-647-16 (1-2095) x US-08-847-844A-80 (1-10)

QY 1164 GGAGTGGGCTGCTGCC 1181
DB 4 GlyValGlyLeuLeuSer 9

RESULT 23
US-09-220-528-91
Sequence 91, Application US/09220528A
Patent No. 6284540
GENERAL INFORMATION:
APPLICANT: Milbrandt, Jeffrey D.
APPLICANT: Baloh, Robert H.
TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor
FILE REFERENCE: 6029-7998
CURRENT APPLICATION NUMBER: US/09/220,528A
CURRENT FILING DATE: 1998-12-24
EARLIER APPLICATION NUMBER: 09/218,698
EARLIER FILING DATE: 1998-12-22
EARLIER APPLICATION NUMBER: 60/108,148
EARLIER FILING DATE: 1998-11-12
EARLIER APPLICATION NUMBER: 09/163,283
EARLIER FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 120
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 91
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-09-220-528-91

Alignment Scores:
Pred. No.: 5.37e+03
Score: 6.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0.86%
Indels: 0
Gaps: 0
DB:
US-09-824-647-16 (1-2095) x US-09-220-528-91 (1-10)

QY 1325 ACCCCAGACATCGGCT 1342
DB 2 ThrProGluThrSerAla 7

RESULT 24
US-09-099-543C-27
Sequence 27, Application US/09099543C
Patent No. 6326200
GENERAL INFORMATION:
APPLICANT: Valmori, Danila

RESULT 26
US-08-672-850-19
; Sequence 19, Application US/08672850
; Patent No. 6140117
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey
; APPLICANT: Araki, Toshiyuki
; TITLE OF INVENTION: NINJURIN
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,850
; FILING DATE: 24-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.
; REGISTRATION NUMBER: 38,304
; REFERENCE/DOCKET NUMBER: A-63610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-672-850-19
Alignment Scores:
Pred. No.: 5.21e+03 Length: 12
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.87% Indels: 0
DB: 4 Gaps: 0
US-09-824-647-16 (1-2095) x US-08-672-850-19 (1-12)
QY 1946 GGCCTTAGATGAGGCC 1929
Db 5 GlyLeuArgLeuArgPro 10
RESULT 27
US-08-726-306A-161
; Sequence 161, Application US/08726306A
; Patent No. 5958684
; GENERAL INFORMATION:
; APPLICANT: van Leeuwen, Frederik Willem
; APPLICANT: Burbach, Johannes Peter Henri
; APPLICANT: Grosveld, Franklin G.
; TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
; NUMBER OF SEQUENCES: 189
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1 Financial Center
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,306A
FILING DATE: 02-Oct-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 95/20080.4
FILING DATE: 02-Oct-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,832
FILING DATE: 01-Jan-1996
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 161:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-726-306A-161
Alignment Scores:
Pred. No.: 5.15e+03 Length: 13
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.87% Indels: 0
DB: 2 Gaps: 0
US-09-824-647-16 (1-2095) x US-08-726-306A-161 (1-13)
QY 1663 AGACGCCTGGCGTAGG 1646
Db 4 ArgArgProGlyArgArg 9
RESULT 28
US-08-602-999A-82
; Sequence 82, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A

us-09-824-647-16.lim.ra1

Tue Jul 8 07:45:07 2003

```

; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MISTOCK, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-82

Alignment Scores:
Pred. No.: 5.15e+03 Length: 13
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.87% Indels: 0
DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x US-08-602-999A-82 (1-13)

Qy 1513 AGACCACTTCCTTCGC 1496
Db 4 ArgProLeuProSerArg 9

RESULT 29
US-08-278-865-82
; Sequence 82, Application US/08278865
; Patent No. 6303574
; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.
; APPLICANT: SPARKS, ANDREW B.
; APPLICANT: THORN, JUDITH M.
; APPLICANT: QUILLIAM, LAWRENCE A.
; APPLICANT: DER, CHANNING J.
; TITLE OF INVENTION: SRC SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/278,865
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-007-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-278-865-82

Alignment Scores:
Pred. No.: 5.15e+03 Length: 13
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-183-841-4 (1-13)

Qy 580 AGTGTCCCACTGGGAAGT 697
Db 2 SerCysProValGlyser 7

RESULT 31
US-09-500-124-82
; Sequence 82, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York

```

;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/500,124
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/602,999
;; FILING DATE: 16-FEB-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Misrock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-202
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 82:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 13 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-09-500-124-82

Alignment Scores: 5.15e+03 Length: 13
Pred. No.: 6.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 0.87% Gaps: 0
DB: 4

US-09-824-647-16 (1-2095) x US-09-500-124-82 (1-13)

QY 1513 AGACCACTTCCTTCGC 1496
Db |||||||||||||||
4 ArgProLeuProSerArg 9

RESULT 32
US-08-766-596A-40
Sequence 40, Application US/08/66596A
Patent No. 6462171
GENERAL INFORMATION:
APPLICANT: SOTO-JARA, Claudio
APPLICANT: BADMANN, Marc
APPLICANT: FRANGONE, Blas
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
TITLE OF INVENTION: DEPOSITS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:
CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/630,645
;; FILING DATE: 10-APR-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/478,326
;; FILING DATE: 06-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: YUN, Allen C.
;; REGISTRATION NUMBER: 37,971
;; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; INFORMATION FOR SEQ ID NO: 40:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 13 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-766-596A-40

Alignment Scores: 5.15e+03 Length: 13
Pred. No.: 6.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 0.86% Gaps: 0
DB: 4

US-09-824-647-16 (1-2095) x US-08-766-596A-40 (1-13)

QY 1631 GCTGGCCCTGCTGCTCCCT 1648
Db |||||||||||||||
7 AlaGlyProAlaValPro 12

RESULT 33
US-08-445-745-120
Sequence 120, Application US/08445745
Patent No. 5672585
GENERAL INFORMATION:
APPLICANT: Pierschbacher, Michael D.
APPLICANT: Cheng, Soan
APPLICANT: Craig, William S.
APPLICANT: Tschopp, Juerg F.
TITLE OF INVENTION: Methods and Composition for Treating
TITLE OF INVENTION: Thrombosis
NUMBER OF SEQUENCES: 168
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,745
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/171,068
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: US 08/079,441
FILING DATE: 18-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,73614
FILING DATE: 14-APR-1993
PRIOR APPLICATION DATA:

us-09-824-647-16.lim.ra1

Tue Jul 8 07:45:07 2003

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; APPLICATION NUMBER: US 07/681,119
; FILING DATE: 05-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/506,444
; FILING DATE: 06-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9829
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 120:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 2
; OTHER INFORMATION: /note= "Xaa = (orn)"
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US-08-445-745-120
Alignment Scores:
Pred. No.: 5.09e+03 Length: 14
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.87% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x US-08-445-745-120 (1-14)
QY 653 CGGACCTGCTGGCGGA 636
DB 9 ArgAspArgAlaSerGly 14

RESULT 34
US-09-120-365-82
; Sequence 82, Application US/09120365
; Patent No. 6103514
; GENERAL INFORMATION:
; APPLICANT: Natori, Shunji
; TITLE OF INVENTION: NEW PROTEASE
; FILE REFERENCE: 32290-144749
; CURRENT APPLICATION NUMBER: US/09/120,365
; CURRENT FILING DATE: 1998-07-22
; EARLIER FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 82
; LENGTH: 14
; TYPE: PRT
; ORGANISM: murine
US-09-120-365-82
Alignment Scores:
Pred. No.: 5.09e+03 Length: 14
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 3 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-120-365-82 (1-14)
QY 1270 AGCGATCGTGGCTGGA 1287
DB 6 SerGluIleValAlaGly 11

RESULT 35
US-09-120-365-83
; Sequence 83, Application US/09120365
; Patent No. 6103514
; GENERAL INFORMATION:
; APPLICANT: Natori, Shunji
; TITLE OF INVENTION: NEW PROTEASE
; FILE REFERENCE: 32290-144749
; CURRENT APPLICATION NUMBER: US/09/120,365
; CURRENT FILING DATE: 1998-07-22
; EARLIER FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 83
; LENGTH: 14
; TYPE: PRT
; ORGANISM: rattus
US-09-120-365-83
Alignment Scores:
Pred. No.: 5.09e+03 Length: 14
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 3 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-120-365-83 (1-14)
QY 1270 AGCGATCGTGGCTGGA 1287
DB 6 SerGluIleValAlaGly 11

RESULT 36
US-09-120-365-84
; Sequence 84, Application US/09120365
; Patent No. 6103514
; GENERAL INFORMATION:
; APPLICANT: Natori, Shunji
; TITLE OF INVENTION: NEW PROTEASE
; FILE REFERENCE: 32290-144749
; CURRENT APPLICATION NUMBER: US/09/120,365
; CURRENT FILING DATE: 1998-07-22
; EARLIER FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 84
; LENGTH: 14
; TYPE: PRT
; ORGANISM: bovine
US-09-120-365-84
Alignment Scores:
Pred. No.: 5.09e+03 Length: 14
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 3 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-120-365-84 (1-14)
QY 1270 AGCGATCGTGGCTGGA 1287
DB 6 SerGluIleValAlaGly 11

RESULT 37
US-09-120-365-86
; Sequence 86, Application US/09120365
; Patent No. 6103514
; GENERAL INFORMATION:
; APPLICANT: Natori, Shunji
; TITLE OF INVENTION: NEW PROTEASE

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; FILE REFERENCE: 32290-144749
; CURRENT APPLICATION NUMBER: US/09/120,365
; CURRENT FILING DATE: 1998-07-22
; EARLIER APPLICATION NUMBER: JP 9-333 474
; EARLIER FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 14
; TYPE: PRT
; ORGANISM: chicken
US-09-120-365-86
Alignment Scores:
Pred. No.: 14 Length: 5.09e+03
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 3 Gaps: 0
US-09-824-647-16 (1-2095) x US-09-120-365-86 (1-14)
QY 1270 AGCGAGATCGTGCTGGA 1287
Db 6 SerGlulIleValAlaGly 11
RESULT 38
US-09-515-039-82
; Sequence 82, Application US/09515039
; Patent No. 6214599
; GENERAL INFORMATION:
; APPLICANT: Natori, Shunji
; TITLE OF INVENTION: NEW PROTEASE
; FILE REFERENCE: 32290-144749
; CURRENT APPLICATION NUMBER: US/09/515,039
; CURRENT FILING DATE: 2000-03-06
; EARLIER APPLICATION NUMBER: JP 9-333 474
; EARLIER FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 14
; TYPE: PRT
; ORGANISM: murine
US-09-515-039-82
Alignment Scores:
Pred. No.: 14 Length: 5.09e+03
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 4 Gaps: 0
US-09-824-647-16 (1-2095) x US-09-515-039-82 (1-14)
QY 1270 AGCGAGATCGTGCTGGA 1287
Db 6 SerGlulIleValAlaGly 11
RESULT 39
US-09-515-039-83
; Sequence 83, Application US/09515039
; Patent No. 6214599
; GENERAL INFORMATION:
; APPLICANT: Natori, Shunji
; TITLE OF INVENTION: NEW PROTEASE
; FILE REFERENCE: 32290-144749
; CURRENT APPLICATION NUMBER: US/09/515,039
; CURRENT FILING DATE: 2000-03-06
; EARLIER APPLICATION NUMBER: JP 9-333 474
; EARLIER FILING DATE: 1997-11-18
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; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 14
; TYPE: PRT
; ORGANISM: rattus
US-09-515-039-83
Alignment Scores:
Pred. No.: 14 Length: 5.09e+03
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 4 Gaps: 0
US-09-824-647-16 (1-2095) x US-09-515-039-83 (1-14)
QY 1270 AGCGAGATCGTGCTGGA 1287
Db 6 SerGlulIleValAlaGly 11
RESULT 40
US-09-515-039-84
; Sequence 84, Application US/09515039
; Patent No. 6214599
; GENERAL INFORMATION:
; APPLICANT: Natori, Shunji
; TITLE OF INVENTION: NEW PROTEASE
; FILE REFERENCE: 32290-144749
; CURRENT APPLICATION NUMBER: US/09/515,039
; CURRENT FILING DATE: 2000-03-06
; EARLIER APPLICATION NUMBER: JP 9-333 474
; EARLIER FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 14
; TYPE: PRT
; ORGANISM: bovine
US-09-515-039-84
Alignment Scores:
Pred. No.: 14 Length: 5.09e+03
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 4 Gaps: 0
US-09-824-647-16 (1-2095) x US-09-515-039-84 (1-14)
QY 1270 AGCGAGATCGTGCTGGA 1287
Db 6 SerGlulIleValAlaGly 11
RESULT 41
US-09-515-039-86
; Sequence 86, Application US/09515039
; Patent No. 6214599
; GENERAL INFORMATION:
; APPLICANT: Natori, Shunji
; TITLE OF INVENTION: NEW PROTEASE
; FILE REFERENCE: 32290-144749
; CURRENT APPLICATION NUMBER: US/09/515,039
; CURRENT FILING DATE: 2000-03-06
; EARLIER APPLICATION NUMBER: JP 9-333 474
; EARLIER FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 14
; TYPE: PRT
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us-09-824-647-16.lim.ra1

Tue Jul 8 07:45:07 2003

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; ORGANISM: chicken
US-09-515-039-86

Alignment Scores:
Pred. No.: 5.09e+03 Length: 14
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-515-039-86 (1-14)

QY 1270 AGCAGATCGTGGTGA 1287
DB 6 SerGluIleValAlaGly 11

RESULT 42
US-09-400-653A-11
; Sequence 11, Application US/09400653A
; Patent No. 6348311
; GENERAL INFORMATION:
; APPLICANT: Kastan, Michael
; APPLICANT: Canman, Christine
; APPLICANT: Kim, Seong-Tae
; APPLICANT: Lim, Dae-Sik
; APPLICANT: St. Jude Children's Research Hospital
; TITLE OF INVENTION: ATM Kinase Modulation for Screening and Therapies
; FILE REFERENCE: 2427/Of142
; CURRENT APPLICATION NUMBER: US/09/400,653A
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: 09/248,061
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-400-653A-11

Alignment Scores:
Pred. No.: 5.09e+03 Length: 14
Score: 6.00 Matches: 6
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.87% Indels: 0
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QY 1468 AGCCAGCGGCGAGCAGT 1451
DB 7 SerGlnProGlySerSer 12

RESULT 43
US-09-302-305C-4
; Sequence 4, Application US/09302305C
; Patent No. 6350572
; GENERAL INFORMATION:
; APPLICANT: Bernards, Rene
; APPLICANT: Zwijsen, Renate
; TITLE OF INVENTION: Interaction Between Cyclin D1 and Steroid Receptor
; FILE REFERENCE: 4238/80713
; CURRENT APPLICATION NUMBER: US/09/302,305C
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT/GB99/00440
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-302-305C-4

Alignment Scores:
Pred. No.: 5.09e+03 Length: 14
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
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DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-302-305C-4 (1-14)

QY 1131 CTCCTCCGATACCTGCTG 1148
DB 5 LeuLeuArgTyrLeuLeu 10

RESULT 44
US-09-302-305C-17
; Sequence 17, Application US/09302305C
; Patent No. 6350572
; GENERAL INFORMATION:
; APPLICANT: Bernards, Rene
; APPLICANT: Zwijsen, Renate
; TITLE OF INVENTION: Interaction Between Cyclin D1 and Steroid Receptor
; FILE REFERENCE: 4238/80713
; CURRENT APPLICATION NUMBER: US/09/302,305C
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT/GB99/00440
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-302-305C-17

Alignment Scores:
Pred. No.: 5.09e+03 Length: 14
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US-09-824-647-16 (1-2095) x US-09-302-305C-17 (1-14)

QY 1131 CTCCTCCGATACCTGCTG 1148
DB 5 LeuLeuArgTyrLeuLeu 10

RESULT 45
US-09-248-061B-9
; Sequence 9, Application US/09248061B
; Patent No. 6387640
; GENERAL INFORMATION:
; APPLICANT: Kastan, M.
; APPLICANT: Canman, C.
; APPLICANT: Kim, S.-T.
; APPLICANT: Lim, D.-S.
; APPLICANT: St. Jude Children's Research Hospital
; TITLE OF INVENTION: ATM Kinase Modulation for Screening and Therapies
; FILE REFERENCE: 2427/Of142
; CURRENT APPLICATION NUMBER: US/09/248,061B
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-248-061B-9

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-248-061B-9

Alignment Scores:
Pred. No.: 5.09e+03 Length: 14
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
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US-09-824-647-16 (1-2095) x US-09-248-061B-9 (1-14)

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Db |||||||||||||||
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Search completed: July 7, 2003, 16:09:34
Job time : 33 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: July 7, 2003, 15:47:40 ; Search time 24 Seconds
(without alignments)
5136.752 Million cell updates/sec

Title: US-09-824-647-16

Perfect score: 694

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-DB-issued Patents AA -OFFMT-fastan -SUFFIX-std.ra1 -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-bits -START-1 -END-1 -MATRIX-oligo -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-quality -THR_MIN-1 -ALIGN-45 -MODE-LOCAL
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-NO_MAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-60 -XGAPEXT-60 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-60 -YGAPEXT-60 -DELOP-6 -DELEXT-7

Database : Issued Patents AA: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	593	85.4	593	US-08-991-862-17	Sequence 17, Appl
2	406	58.5	593	US-07-668-648-4	Sequence 4, Appli
3	406	58.5	593	US-08-429-998-4	Sequence 4, Appli
4	406	58.5	593	US-08-431-333-4	Sequence 4, Appli
5	406	58.5	593	PCT-US91-02321-4	Sequence 4, Appli
6	32	4.6	589	US-07-668-648-2	Sequence 2, Appli
7	32	4.6	589	US-07-668-648-6	Sequence 6, Appli
8	32	4.6	589	US-08-429-998-2	Sequence 2, Appli
9	32	4.6	589	US-08-429-998-6	Sequence 6, Appli
10	32	4.6	589	US-08-431-333-2	Sequence 2, Appli
11	32	4.6	589	US-08-431-333-6	Sequence 6, Appli
12	32	4.6	589	US-08-991-862-2	Sequence 2, Appli

13	32	4.6	589	5	PCT-US91-02321-2	Sequence 2, Appli
14	32	4.6	589	5	PCT-US91-02321-6	Sequence 6, Appli
15	15	2.7	19	4	US-08-991-862-6	Sequence 6, Appli
16	16	2.3	179	1	US-07-668-648-8	Sequence 8, Appli
17	16	2.3	179	2	US-08-429-998-8	Sequence 8, Appli
18	16	2.3	179	2	US-08-431-333-8	Sequence 8, Appli
19	16	2.3	179	5	PCT-US91-02321-8	Sequence 8, Appli
20	14	2.0	14	4	US-08-991-862-7	Sequence 7, Appli
21	11	1.6	15	1	US-08-245-853-2	Sequence 2, Appli
22	11	1.6	15	1	US-08-573-675-2	Sequence 2, Appli
23	11	1.6	15	6	5470825-2	Patent No. 5470825
24	8	1.2	29	4	US-09-060-756-732	Sequence 732, App
25	8	1.2	151	3	US-08-584-031-11	Sequence 11, Appl
26	8	1.2	193	1	US-08-106-507-2	Sequence 2, Appli
27	8	1.2	216	1	US-08-106-507-10	Sequence 10, Appl
28	8	1.2	216	1	US-08-446-922-8	Sequence 8, Appli
29	8	1.2	216	5	PCT-US93-10034-8	Sequence 8, Appli
30	8	1.2	230	2	US-08-844-120-3	Sequence 3, Appli
31	8	1.2	230	2	US-09-022-940-3	Sequence 3, Appli
32	8	1.2	230	2	US-09-022-940-5	Sequence 5, Appli
33	8	1.2	230	3	US-09-216-001-3	Sequence 3, Appli
34	8	1.2	230	3	US-09-216-386-3	Sequence 3, Appli
35	8	1.2	230	3	US-09-216-386-5	Sequence 5, Appli
36	8	1.2	230	4	US-08-878-862-3	Sequence 3, Appli
37	8	1.2	230	4	US-09-213-394-3	Sequence 3, Appli
38	8	1.2	257	4	US-09-372-422A-28	Sequence 28, Appl
39	8	1.2	272	4	US-09-372-422A-26	Sequence 26, Appl
40	8	1.2	302	4	US-09-282-305-14	Sequence 14, Appl
41	8	1.2	305	4	US-09-282-305-12	Sequence 12, Appl
42	8	1.2	318	4	US-09-060-756-727	Sequence 727, App
43	8	1.2	401	2	US-08-805-118-1	Sequence 1, Appli
44	8	1.2	401	4	US-09-391-958-1	Sequence 1, Appli
45	8	1.2	480	2	US-08-724-394A-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-08-991-862-17
; Sequence 17, Application US/08991862
; Patent No. 6309826
; GENERAL INFORMATION:
; APPLICANT: Serrieto, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: Z9996.488/P001-A
; CURRENT APPLICATION NUMBER: US/08/991,862
; CURRENT FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/863,862
; EARLIER FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Human GP88 cDNA
US-08-991-862-17

Alignment Scores:
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Score: 593.00 Matches: 593
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.45% Indels: 0
DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x US-08-991-862-17 (1-593)

QY	13	ATGTGACCTGTGTGAGCTGGTGGCTTAACACAGCGGTGGTGGTGAACGCGTGC 72
DB	1	MetTrpThreuValserTrpValAlaLeuThrAlaGlyLeuValAlaGlyThrArgCys 20
QY	73	CCAGATGGTCAGTTCCTGGCCCTGTGGCTGTGTGGCTGGAGCCCGAGGACGACGTACAGC 132

Db	21	ProAspGlyGlnPheCysProValAlaCysCysLeuAspProGlyGlyAlaSerTyrSer	40
QY	133	TGTCGCGTCCCTTCTGCACAAATGGCCCAACAACTCAGCAGGATCTGGGTGGCCCC	192
Db	41	CysCysArgProLeuLeuAspLysTrpProThrThrLeuSerArgHisLeuGlyGlyPro	60
QY	193	TGCCAGGTGATGCCACATGCTCTGCCGGCGCACTCCTGCAATCTTTACCGTCTCAGGGACT	252
Db	61	CysGlnValAspAlaHisCysSerAlaGlyHisSerCysIlePheThrValSerGlyThr	80
QY	253	TTCCAGTTGTCGCCCTTCCAGAGCGCGTGGCATCGGGGATGGCCATCATTCTGTCGCCCA	312
Db	81	SerSerCysCysProPheProGlnAlaValAlaCysGlyAspGlyHisHisCysCysPro	100
QY	313	CGGGGTCCACTGCAGTCGACAGCGGCGATCCTGTTCCAAAGATCAGTAACTCC	372
Db	101	ArgGlyPheHisCysSerAlaAspGlyArgSerCysPheGlnArgSerGlyAsnAsnSer	120
QY	373	GTGGGTGCCATCCAGTCGCGCCTGATAGTCAAGTTCGAATCCCGGACTTTCACAGTCTGT	432
Db	121	ValGlyAlaIleGlnCysProAspSerGlnPheGluCysProAspPheSerThrCysCys	140
QY	433	GTATGCTCGATGGCTTCCTGGGGTCTGCCCCATGCCACCGCTTCCTGCTGTGGAGAC	492
Db	141	ValMetValAspGlySerTrpGlyCysCysProMetProGlnAlaSerCysCysGluAsp	160
QY	493	AGGGTCACCTGCTGTCGGCACGGTGCCTTCTCGACTGTTTCACACCCGCTGCATCAC	552
Db	161	ArgValHisCysCysProHisGlyAlaPheCysAspLeuValHisThrArgCysIleThr	180
QY	553	CCACGGGCACCCCTGGCAAGAAAGCTCCCTGCCCGAGGACTAACAGGCGAGTG	612
Db	181	ProThrGlyThrHisProLeuAlaLysLysLeuProAlaGlnArgThrAsnArgAlaVal	200
QY	613	GCCTTGTCCAGTCGCGTCATGTCTCGGAGCGACGGTCCGGTGCCTGATGGTCTTACC	672
Db	201	AlaLeuSerSerValMetCysProAspAlaArgSerArgCysProAspGlySerThr	220
QY	673	TGCTGTGAGTCGCCAGTGGGAAGTAGTGGCTGTGCTGCCAATGCCAACGCCACTGCTGC	732
Db	221	CysCysGluLeuProSerGlyLysTyrGlyCysCysProMetProAsnAlaThrCysCys	240
QY	733	TCCGATCACCTGCATGCTGCCCCCAAGACATGTGTGTGCACTGTATCCAGAGTAAGTGC	792
Db	241	SerAspHisLeuHisCysCysProGlnAspThrValCysAspLeuIleGlnSerLysCys	260
QY	793	CTCTCCAGAGAACCTTACCAGCGACCTCCTCACTAAGTGCCTCGGCACACAGTGGGC	852
Db	261	LeuSerLysGluAsnAlaThrThrAspLeuLeuThrLysLeuProAlaHisThrValGly	280
QY	853	GATGTGAATGTGACATGGAGTGAGCTGCCAGATGGCTATACCTGCTGCCCTCTACAG	912
Db	281	AspValLysCysAspMetGluValSerCysProAspGlyTyrThrCysCysArgLeuGln	300
QY	913	TCGGGGGCTTGGGGCTGCTGCCCTTTTACCCAGGCTGTGTGTGTGAGGACCAATACAC	972
Db	301	SerGlyAlaTrpGlyCysCysProPheThrGlnAlaValCysCysGluAspHisIleHis	320
QY	973	TGCTGTCCCGGGGTTTACGTGTGACACGACAGGCTACCTGTGAACAGGGGGCCCCAC	1032
Db	321	CysCysProAlaGlyPheThrCysAspThrGlnLysGlyThrCysGluGlnGlyProHis	340
QY	1033	CAGTGGCTTGGATGGAGAGGCCACCGCTCACCTCAGCTGGCCAGACCCACAAAGCTTG	1092
Db	341	GlnValProTrpMetGluLysAlaProAlaHisLeuSerLeuProAspProGlnAlaLeu	360
QY	1093	AAGAGAGATGTCCTTGTGATAATGTGCAGCAGCTGTCCCTCTCCGATACCTGCTGCCAA	1152
Db	361	LysArgAspValProCysAspAsnValSerSerCysCysProSerSerAspThrCysCysGln	380
QY	1153	CTCACGTCTGGGAGTGGGGCTGCTGTCCAAATCCCAAGAGCTGTCTGTCTCGGACCAC	1212
Db	381	LeuThrSerGlyLutrpGlyCysCysProIleProGluAlaValCysCysSerAspHis	400

1213	QY	CAGCACTGCTGCCCCAGCCATACACGTGTGTAGCTGAGGGCGAGTGTCTCAGCGAGGAAC	1272
401	Db	GlnHisCysCysProGlnArgTyrThrCysValAlaGluGlyClnCysGlnAArgGlySer	420
1273	QY	GAGATCGTGGCTGGACTGGAGAGATGCTGTGCCCGCGGGTTCCTATCCACCCACCCAGA	1332
421	Db	GlulleValAlaGlyLeuGluLysMetProAlaAArgGlySerLeuSerHisProArg	440
1333	QY	GACATCGGTGTACACGACACACACCTGCCCGGTGGCGGACCTGCTGCCCGAGCCAG	1392
441	Db	AspIleGlyCysAspGlnHisThrSerCysProValGlyGlyThrCysCysProSerGln	460
1393	QY	GGTGGAGCTGGCGCCCTGCTGCCAGTTGCCCATGCTGTGTCGCAGAGATCCCGACGAC	1452
461	Db	GlyGlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGlnAspArgGlnHis	480
1453	QY	TGCTGCCCGCTGGCTACACCTGCACAGTCGAGGCTCGATCTCCGAGAGAGGAGTGGTC	1512
481	Db	CysCysProAlaGlyTyrThrCysAsnValLysAlaAArgSerCysGluLysGluValVal	500
1513	QY	TCGTGCCAGCTGCCACCTTCCTGGCCCGTAGCCCTCAGCTGGGTGTGAAGGACGTGGAG	1572
501	Db	SerAlaGlnProAlaThrPheLeuAlaAArgSerProHisValGlyValLysAspValGlu	520
1573	QY	TGTGGGGAGGACACTTCCTGCCCATGATACACGACACTGCTGCCGAGACACCCACAGGGC	1632
521	Db	CysGlyGluGlyHisPheCysHisAspAsnGlnThrCysCysArgAspAsnArgGlnGly	540
1633	QY	TGGGCTGCTGTCCCTACGCCACGAGCGTCTGTGTGCTGATCGCGGCCACTGCTGTCCCT	1692
541	Db	TrpAlaCysCysProTyrAlaGlnGlyValCysCysAlaAspArgArgHisCysCysPro	560
1693	QY	GCTGGCTTCGCTGCCGACGAGGGGTACCAAGTGTGTGCGCAGGAGGGCCCGCGCTGG	1752
561	Db	AlaGlyPheArgCysAlaAArgArgGlyThrLysCysLeuAArgGluAlaProAArgTrp	580
1753	QY	GACGCCCTTTGAGGACCCAGCCTTGAGACAGCTGCTG	1791
581	Db	AspAlaProLeuAArgAspProAlaLeuAArgGlnLeuLeu	593

RESULT 2

US-07-668-648-4
US-07-668-648-4
; Sequence 4, Application US/07668648
; Patent No. 5416192
; GENERAL INFORMATION:
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Plowman, Gregory D.
; TITLE OF INVENTION: EPIITHELINS: NOVEL CYSTEINE-RICH GROWTH
; TITLE OF INVENTION: MODULATING PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/668,648
; FILING DATE: 19910819
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-161-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090

Alignment Scores:

Pred. No.: 0 Length: 593
Score: 406.00 Matches: 406
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 58.50% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x US-08-429-998-4 (1-593)

Qy 13 ATGTGGACCTGGTGGAGCTGGTGGCTTAACAGCAGGCTGGTGGCTGGAACGGCTGC 72
Db 1 MetThrLeuValSerTrpValAlaLeuThraAlaGlyLeuValAlaGlyThrArgCys 20
Qy 73 CCAGATGGTCAAGTTCGCTGGCTGGCTGGCTGGACCCCGAGAGAGCCAGCTACAGC 132
Db 21 ProAspGlyGlnPheCysProValAlaCysLeuAspProGlyGlyAlaSerTyrSer 40
Qy 133 TGTCTGCGCTCCCTTCCTGGCAATGGCCACAACTAGCAGGCACTCTGGTGGCCCC 192
Db 41 CysCysArgProLeuLeuAspLysTrpProThrLeuSerArgHisLeuGlyGlyPro 60
Qy 193 TCCAGAGTGTATGCCACTGCTCTGCCGGCCACTTCTGCATCTTACCTGCTCAGGACT 252
Db 61 CysGlnValAspAlaHisCysSerAlaGlyHisSerCysLysPheThrValSerGlyThr 80
Qy 253 TCCAGTTCCTCCCTTCCTCCAGAGCCGCTGGCATGCCGGATGCCATCACTGCTGCCA 312
Db 81 SerSerCysCysProPheProGluAlaValAlaCysGlyAspGlyHisCysCysPro 100
Qy 313 CGGGCTTCCACTGCTGACGAGCGGCGGCTCTGCTTCCAAAGATCAGGTAACAATCC 372
Db 101 ArgGlyPheHisCysSerAlaAspGlyArgSerCysPheGlnArgSerGlyAsnSer 120
Qy 373 GTGGTGCCTCCAGTGCCTGTAGTCAAGTTCGAATGCCCGGACTTCTCCAGCTGCTGT 432
Db 121 ValGlyAlaIleGlnCysProAspSerGlnPheGluCysProAspPheSerThrCysCys 140
Qy 433 GTATGGTCGATGGCTCTGGGGTGGTGGCTGGCCAGCTGCCAGGCTCTGCTGTGAGAC 492
Db 141 ValMetValAspGlySerTrpGlyCysCysProMetProGlnAlaSerCysGlyAsp 160
Qy 493 AGGGTGCCTGCTGCTCCAGCGGCTCTTCTGCGACCTGGTTCACACCGCTGCATCACA 552
Db 161 ArgValHisCysCysProHisGlyAlaPheCysAspLeuValHisThrArgCysLys 180
Qy 553 CCCAGGGGACCCACCCCTCCGCAAGAGCTCCCTGCCAGAGACTAACAGGCGCAGTG 612
Db 181 ProThrGlyThrHisProLeuAlaLysLysLeuProAlaGlnArgThrAsnArgAlaVal 200
Qy 613 GCCTTGTCCAGCTCGTCAATGTCTCGGACGCGCTCCCGTCCCGTGGCTGCTGCTAC 672
Db 201 AlaLeuSerSerValMetCysProAspAlaArgSerArgCysProAspGlySerThr 220
Qy 673 TGTCTGAGCTCCCGAGTGGAGTATGCTGCTGCCCAATGCCCAAGCCACCTGCTGC 732
Db 221 CysCysGluLeuProSerGlyLysTyrGlyCysCysProMetProAsnAlaThrCysCys 240
Qy 733 TCCGATCACTGCTGCTGCCCCCAAGACACTGTGTGTACCTGATCCAGATGAAGTGC 792
Db 241 SerAspHisLeuHisCysCysProGlnAspThrValCysAspLeuIleGlnSerLysCys 260
Qy 793 CTCTCCAGGAACGCTACACGACCTCTCTCACTAAGCTGCTGCCGACACAGTGGGC 852
Db 261 LeuSerLysGluAsnAlaThrThrAspLeuLeuThrLysLeuProAlaHisThrValGly 280
Qy 853 GATGTGAATGTGACATGGAGTGGAGCTGCCAGATGGCTATACCTGCTGCCGCTACAG 912
Db 281 AspValLysCysAspMetGluValSerCysProAspGlyTyrThrCysCysArgLeuGln 300
Qy 913 TCGGGGGCTGGGGTGTGCGCCCTTTTACCAAGGCTGTGCTGTGAGGACACATACAC 972

Db 301 SerGlyAlaTrpGlyCysCysProPheThrGlnAlaValCysCysGluAspHisLeHis 320
Qy 973 TGTGTCTCCCGGGGTTTACGTGTGACACGACGAGGAGGTACCTGTGAACAGGGGCCAC 1032
Db 321 CysCysProAlaGlyPheThrCysAspThrGlnLysGlyThrCysGluGlnGlyProHis 340
Qy 1033 CAGGTGCTGGATGGAGAGGCGCCAGCTCAGCTCAGCTGCGCAGACCCACAGCCTTG 1092
Db 341 GlnValProTrpMetGluLysAlaProAlaHisLeuSerLeuProAspProGlnAlaLeu 360
Qy 1093 AAGAGAGATGTCCTCTGTGATAATGTACAGAGCTGTCTCTCTCCGATACCTGCTGCCAA 1152
Db 361 LysArgAspValProCysAspAsnValSerSerCysProSerSerAspThrCysCysGln 380
Qy 1153 CTCACGCTGGGAGTGGGCTGTCTCAATGCCAGAGGCTGTCTGCTGCTGCGACAC 1212
Db 381 LeuThrSerGlyGluTrpGlyCysCysProIleProGluAlaValCysCysSerAspHis 400
Qy 1213 CAGCAGCTGCTGCCCCAG 1230
Db 401 GlnHisCysCysProGln 406

RESULT 4
US-08-431-333-4
; Sequence 4, Application US/08431333
; Patent No. 5965723
; GENERAL INFORMATION:
; APPLICANT: Shoyab, Mohammed
; APPLICANT: PLOWMAN, Gregory D.
; TITLE OF INVENTION: EPITHELIALS: NOVEL CYSTEINE-RICH GROWTH
; TITLE OF INVENTION: MODULATING PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,333
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/668,648
; FILING DATE: 13-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-161-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212) 869-9741
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 593 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-431-333-4

Alignment Scores:

Pred. No.: 0 Length: 593
Score: 406.00 Matches: 406
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 58.50% Indels: 0
DB: 2 Gaps: 0

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Db      341  GlnValProTrpMetGluLysAlaProAlaHisLeuSerLeuProAspProGlnAlaLeu 360
Qy      1093  AAGAGAGATGTCCTCTGTGATAATGTCTCAGCAGCTGTCTCCTCTCCGATACCTCTGTCGCAA 1152
Db      361  LysArgAspValProCysAspAsnValSerSerCysProSerSerAspThrCysCysGln 380
Qy      1153  CTCAGTCTGGGAGTGGGCTGTCTGCCAATCCAGAGGCTGTCTGCTCGGACAC 1212
Db      381  LeuThrSerGlyGluTrpGlyCysCysProIleProGluAlaValCysCysSerAspHis 400
Qy      1213  CAGCAGTGTCTGCCCCCAG 1230
Db      401  GlnHisCysCysProGln 406

RESULT 5
PCT-US91-02321-4
: Sequence 4, Application PC/TUS9102321
: GENERAL INFORMATION:
: APPLICANT: Shoyab, Mohammed
: TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
: TITLE OF INVENTION: MODULATING PROTEINS
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Bristol-Myers Squibb Company
: STREET: 3005 First Avenue
: CITY: Seattle
: STATE: Washington
: COUNTRY: USA
: ZIP: 98121
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA: PCT/US91/02321
: APPLICATION NUMBER: PCT/US91/02321
: FILING DATE: 19910403
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Poor, Brian W.
: REGISTRATION NUMBER: 32,928
: REFERENCE/DOCKET NUMBER: ON0071A-PC
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)728-4800
: TELEFAX: (206)448-4775
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 593 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: linear
: MOLECULE TYPE: protein
PCT-US91-02321-4

Alignment Scores:
Pred. NO.: 0 Length: 593
Score: 406.00 Matches: 406
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 58.50% Indels: 0
DB: 5 Gaps: 0

US-09-824-647-16 (1-2095) x PCT-US91-02321-4 (1-593)

Qy      13  ATGTGGACCCCTGTGTAGCTGGTGGCCCTTAACACAGCGCTGTGGTGGACCGCGTGC 72
Db      1  MetTrpThrLeuValSerTrpValAlaLeuThrAlaGlyLeuValAlaGlyThrArgCys 20
Qy      73  CCAGATGTCAGTTCTCCCTGTGTGGCTGTCTGCTGCACCCCGGAGGAGCCAGCTACAGC 132
Db      21  ProAspGlyGlnPheCysProValAlaCysCysLeuAspProGlyGlyAlaSerTyrSer 40
Qy      133  TGCTGCCGTGCCCTTCTGGGAAATGCCACAACTGACGACGCAATCTGGGTGGCCCC 192

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Db 401 GlnHisCysCysProGln 406

RESULT 6
US-07-668-648-2
Sequence 2, Application US/07668648
Patent No. 5416192
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plozman, Gregory D.
TITLE OF INVENTION: EPITHELIALS: NOVEL CYSTEINE-RICH GROWTH
MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,648
FILING DATE: 19910819
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 589 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-668-648-2

Alignment Scores:

Pred. No.	Length:
Score:	1.12e-20
Percent Similarity:	32.00
Best Local Similarity:	100.00%
Query Match:	Mismatches: 0
DB:	Indels: 0
	Gaps: 0

US-09-824-647-16 (1-2095) x US-07-668-648-2 (1-589)

Oy 1396 GGGAGCTGGCGCTCTGCCAGTGTCCCGATCTGCCCGTCGCTGCAGGATCGC
Db 460 GlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArg
Oy 1456 TGCCCGCTGGCTACACTGCAACCTGAAGCTCGA 1491
Db 480 CysProAlaGlyThrCysAsnValLysAlaArg 491

RESULT 7
US-07-668-648-6
Sequence 6, Application US/07668648
Patent No. 5416192
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plozman, Gregory D.
TITLE OF INVENTION: EPITHELIALS: NOVEL CYSTEINE-RICH GROWTH
MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds

41 CysCysArgProLeuLeuAspLysTrpProThrLeuSerArgHisLeuGlyGlyPro 60
193 TCCAGGTTGATGCCCATGCTCTGCCGGCCACTCTGATCTTATCGTCTCAGGACT 252
61 CysGlnValAspAlaHisCysSerAlaGlyHisSerCysIlePheThrValSerGlyThr 80
253 TCAGTTGCTGCCCTTCCCAGAGCCCTGGCATGGGGATGGCCATCAGTCTGCCCA 312
81 SerSerCysCysProPheProGluAlaValAlaCysGlyAspGlyHisHisCysCysPro 100
313 CGGGCTTCCACTGAGTGCACAGCGGCGATCTGCTTCCAAGATCAGSTAACAACCTC 372
101 ArgGlyPheHisCysSerAlaAspGlyArgSerCysPheGlnArgSerGlyAsnSer 120
373 GTGGTGCCATCAGTGCCTGATAGTCAGTTCGAAATGCCGGACTCTCCAGTCTCT 432
121 ValGlyAlaIleGlnCysProAspSerGlnPheGluCysProAspPheSerThrCysCys 140
433 GTTAGTGTGAGTCTTGGGGTCTGCCCATGCTGCCCGAGCTCTCTGCTGTGAAGAC 492
141 ValMetValAspGlySerTrpGlyCysCysProMetProGlnAlaSerCysGluAsp 160
493 AGGTGCTGCTGCTCCGACGGTGTCTGCGACTGTGTCACACCGCTCATCACCA 552
161 ArgValHisCysCysProHisGlyAlaPheCysAspLeuValHisThrArgCysIleThr 180
553 CCCAGGGACCACCCCTGGCAAAGACTCCCTGCCAGAGGACTAACAGGGCAGTG 612
181 ProThrGlyThrHisProLeuAlaLysLysLeuProAlaGlnArgThrAsnArgAlaVal 200
613 GCCTTGCTCAGTTCGGTTCGAGTTCGGAGCAGGTCGGGGTCCGCTGATGTTTACC 672
201 AlaLeuSerSerValMetCysProAspAlaArgSerArgCysProAspGlySerThr 220
673 TGCTGTCAGTCCGCTGAGTGGAGTGGCTGCTGCCCAATGCCACGCGCACTGCTGC 732
221 CysCysGluLeuProSerGlyLysTrpGlyCysCysProMetProAsnAlaThrCysCys 240
733 TCCGATCACCTGCACTGCTGCCCAACAGACTGTGTGCTGCTGAGGACACATAC 792
241 SerAspHisLeuHisCysCysProGlnAspThrValCysAspLeuLleGlnSerLysCys 260
793 CTCTCCAGAGAACGCTACACGGACTCTCTACTAGTCTGCTGCCGACACAGTGGC 852
261 LeuSerLysGluAsnAlaThrAspLeuLeuThrLysLeuProAlaHisThrValGly 280
853 GATCTGAATGTGACATGGAGTGGCTGCTGCCAGATGCTGCTGCTGCTGCTACAG 912
281 AspValLysCysAspMetGluValSerCysProAspGlyThrCysCysArgLeuGln 300
913 TCGGGGCTGGGCTGCTGCCCTTTTACCAGGCTGTGCTGTGAGGACACATACAC 972
301 SerGlyAlaTrpGlyCysCysProPheThrGlnAlaValCysCysGluAspHisIleHis 320
973 TCGTGTCCCGGGGTTTACGTGTGACGACGAGGTAAGTCTGTGACAGGCGCCAC 1032
321 CysCysProAlaGlyPheThrCysAspThrGlnLysGlyThrCysGluGlnGlyProHis 340
1033 CAGTGTCCCTGGTGGAGAAGCCCCAGCTACCTCAGCTGCCAGACCCACAGACCTTG 1092
341 GlnValProTrpMetGluLysAlaProAlaHisLeuSerLeuProAspProGluAlaLeu 360
1093 AAGAGATGTCCCTGTGATAATGTACAGAGTGTCTCCCTCTCCGATACCTGCTGCCAA 1152
361 LysArgAspValProCysAspAsnValSerSerCysProSerSerAspThrCysCysGln 380
1153 CTCAGCTGTGGGAGTGGGCTGTGTGTCATTCACAGAGGCTGTGCTGCTGCTCGACAC 1212
381 LeuThrSerGlyGluTrpGlyCysCysProIleProGluAlaValCysCysSerAspHis 400
1213 CAGCACTGCTGCCCGCCAG 1230

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/07/668,648
FILING DATE: 19910819
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 589 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-668-648-6

Alignment Scores:
Pred. No.: 1.12e-20 Length: 589
Score: 32.00 Matches: 32
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.61% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x US-07-668-648-6 (1-589)

QY 1396 GGGAGCTGGGCTGCTGCCAGTTCGCCATGCTGCTGCCAGGATGCCAGCACTGC 1455
|||||
Db 460 GlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHisCys 479
QY 1456 TGCCCGCTGGCTACACTGCAAGTGAAGCTCGA 1491
|||||
Db 480 CysProAlaGlyTyrThrCysAsnValIysAlaArg 491

RESULT 8

US-08-429-998-2
Sequence 2, Application US/08429998
Patent No. 5885961
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Flowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/429,998
FILING DATE: 27-APR-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 589 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-429-998-2

Alignment Scores:
Pred. No.: 1.12e-20 Length: 589
Score: 32.00 Matches: 32
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.61% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x US-08-429-998-2 (1-589)

QY 1396 GGGAGCTGGGCTGCTGCCAGTTCGCCATGCTGCTGCCAGGATGCCAGCACTGC 1455
|||||
Db 460 GlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHisCys 479
QY 1456 TGCCCGCTGGCTACACTGCAAGTGAAGCTCGA 1491
|||||
Db 480 CysProAlaGlyTyrThrCysAsnValIysAlaArg 491

RESULT 9

US-08-429-998-6
Sequence 6, Application US/08429998
Patent No. 5885961
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Flowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,998
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 6:

us-09-824-647-16.std.ra1

Tue Jul 8 07:45:13 2003

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SEQUENCE CHARACTERISTICS:
LENGTH: 589 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-429-998-6
Alignment Scores:
Pred. No.: 1.12e-20 Length: 589
Score: 32.00 Matches: 32
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.61% Indels: 0
DB: Gaps: 0

US-09-824-647-16 (1-2095) x US-08-429-998-6 (1-589)
QY 1396 GGGAGCTGGCGCTGCTGCCAGTTGCCCATGTGCTGTCGAGGATGCCAGCACTGC 1455
Db 460 GlySerTrpAlaCysGlnLeuProHisAlaValCysCysGluaspargGlnHisCys 479
QY 1456 TGGCCGGCTGGCTACACCTGCAACGCTGAAGGCTCGA 1491
Db 480 CysProAlaGlyTyrThrCysAsnValLysAlaArg 491

RESULT 11
US-08-431-333-6
; Sequence 6, Application US/08431333
; Patent No. 5965723
; GENERAL INFORMATION:
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Shoyab, Gregory D.
; TITLE OF INVENTION: EPIITHELINS: NOVEL CYSTEINE-RICH GROWTH
; TITLE OF INVENTION: MODULATING PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431.333
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/668,648
; FILING DATE: 13-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-161-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212) 869-9741
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 589 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-431-333-6
Alignment Scores:
Pred. No.: 1.12e-20 Length: 589
Score: 32.00 Matches: 32
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.61% Indels: 0
DB: Gaps: 0

US-09-824-647-16 (1-2095) x US-08-431-333-6 (1-589)
QY 1396 GGGAGCTGGCGCTGCTGCCAGTTGCCCATGTGCTGTCGAGGATGCCAGCACTGC 1455
Db 460 GlySerTrpAlaCysGlnLeuProHisAlaValCysCysGluaspargGlnHisCys 479
QY 1456 TGGCCGGCTGGCTACACCTGCAACGCTGAAGGCTCGA 1491
Db 480 CysProAlaGlyTyrThrCysAsnValLysAlaArg 491

RESULT 10
US-08-431-333-2
; Sequence 2, Application US/08431333
; Patent No. 5965723
; GENERAL INFORMATION:
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Shoyab, Gregory D.
; TITLE OF INVENTION: EPIITHELINS: NOVEL CYSTEINE-RICH GROWTH
; TITLE OF INVENTION: MODULATING PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431.333
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/668,648
; FILING DATE: 13-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-161-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212) 869-9741
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 589 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-431-333-2
Alignment Scores:
Pred. No.: 1.12e-20 Length: 589
Score: 32.00 Matches: 32
Percent Similarity: 100.00% Conservative: 0

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Db 480 CysProAlaGlyTyrThrCysAsnValLysAlaArg 491

RESULT 12

US-08-991-862-2

Sequence 2, Application US/08991862

Patent No. 6309826

GENERAL INFORMATION:

APPLICANT: Serrero, GINETTE

TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS

FILE REFERENCE: Z9996.488/P001-A

CURRENT APPLICATION NUMBER: US/08/991,862

CURRENT FILING DATE: 1998-08-17

EARLIER APPLICATION NUMBER: 08/863,862

EARLIER FILING DATE: 1997-05-23

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 589

TYPE: PRT

ORGANISM: Mouse epithelin/granulin

US-08-991-862-2

Alignment Scores:
Pred. No.: 1,12e-20 Length: 589
Score: 32.00 Matches: 32
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.61% Indels: 0
DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x US-08-991-862-2 (1-589)

QY 1396 GGGAGCTGGCTGCTGCCAGTGGCCCATGCTGTGCTGCGAGGATGCCAGCACTGC 1455

Db 460 GlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHisCys 479

QY 1456 TGCCCGGCTGCTACACCTGCAACGTGAAGGCTCGA 1491

Db 480 CysProAlaGlyTyrThrCysAsnValLysAlaArg 491

RESULT 13

PCT-US91-02321-2

Sequence 2, Application PC/TUS9102321

GENERAL INFORMATION:

APPLICANT: Shoyab, Mohammed

TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH

FACTORS: MODULATING PROTEINS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bristol-Myers Squibb Company

STREET: 3005 First Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US91/02321

FILING DATE: 19910403

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Poor, Brian W.

REGISTRATION NUMBER: 32,928

REFERENCE/DOCKET NUMBER: ON0071A-PC

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)728-4800

TELEFAX: (206)448-4775

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 589 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US91-02321-2

Alignment Scores:

Pred. No.: 1,12e-20 Length: 589

Score: 32.00 Matches: 32

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 4.61% Indels: 0

DB: 5 Gaps: 0

US-09-824-647-16 (1-2095) x PCT-US91-02321-2 (1-589)

QY 1396 GGGAGCTGGCTGCTGCCAGTGGCCCATGCTGTGCTGCGAGGATGCCAGCACTGC 1455

Db 460 GlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHisCys 479

QY 1456 TGCCCGGCTGCTACACCTGCAACGTGAAGGCTCGA 1491

Db 480 CysProAlaGlyTyrThrCysAsnValLysAlaArg 491

RESULT 14

PCT-US91-02321-6

Sequence 6, Application PC/TUS9102321

GENERAL INFORMATION:

APPLICANT: Shoyab, Mohammed

TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH

FACTORS: MODULATING PROTEINS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bristol-Myers Squibb Company

STREET: 3005 First Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US91/02321

FILING DATE: 19910403

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Poor, Brian W.

REGISTRATION NUMBER: 32,928

REFERENCE/DOCKET NUMBER: ON0071A-PC

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)728-4800

TELEFAX: (206)448-4775

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 589 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US91-02321-6

Alignment Scores:

Pred. No.: 1,12e-20 Length: 589

Score: 32.00 Matches: 32

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 4.61% Indels: 0

DB: 5 Gaps: 0

us-09-824-647-16.std.ra1

Tue Jul 8 07:45:13 2003

```

US-09-824-647-16 (1-2095) x PCT-US91-02321-6 (1-589)
QY 1396 GGGAGCTGGGCTGCTGCACAGTGCACATCTGTGTGCTGGAGGATGCCAGCAGTGC 1455
DB 460 GlySerTrpAlaCysCysGlnProHisAlaValCysCysGluAspArgGlnHisCys 479
QY 1456 TGCCCGGCTGGCTACACCTGCACCTGCACCTGAAGGCTCA 1491
DB 480 CysProAlaGlyTyrThrCysAsnValLysAlaArg 491

RESULT 15
US-08-991-862-6
; Sequence 6, Application US/08991862
; Patent No. 6309826
; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996.488/P001-A
; CURRENT APPLICATION NUMBER: US/08/991,862
; CURRENT FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/863,862
; EARLIER FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Human granulin
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(19)
; OTHER INFORMATION: Internal peptide of human GP88 used to develop
; neutralizing anti-human GP88 monoclonal antibody.
US-08-991-862-6

Alignment Scores:
Pred. No.: 9.66e-09 Length: 19
Score: 19.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.74% Indels: 0
DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x US-08-991-862-6 (1-19)
QY 1048 GAGAAGCCCGCCAGCTCACTCAGCTGCACAGCCACAGCCTTGAAGAGATGTC 1104
DB 1 GluLysAlaProAlaHisLeuSerLeuProAspProGlnAlaLeuLysArgAspVal 19

RESULT 16
US-07-668-648-8
; Sequence 8, Application US/07668648
; Patent No. 5416192
; GENERAL INFORMATION:
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Shoyab, Gregory D.
; TITLE OF INVENTION: EPIITHELINS: NOVEL CYSTEINE-RICH GROWTH
; TITLE OF INVENTION: MODULATING PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/668,648
; FILING DATE: 13-MAR-1991
; PRIORITY APPLICATION NUMBER:
; PRIORITY APPLICATION DATE:
; CLASSIFICATION:
; APPLICANT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-161-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

```


MOLECULE TYPE: protein
US-08-429-998-8

Alignment Scores:
Pred. No.: 3.4e-06 Length: 179
Score: 16.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.31% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x US-08-429-998-8 (1-179)

QY 892 TATACCTGCTGCCTACAGTCGGGGCTGGGGCTGCCTGCTGCTTTT 939
|||||
DB 66 TyrThrCysCysArgLeuGlnSerGlyAlaTrpGlyCysCysProPhe 81
|||||

RESULT 18

US-08-431-333-8
; Sequence 8, Application US/08431333
; Patent No. 5965723
; GENERAL INFORMATION:
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Shoyab, Gregory D.
; TITLE OF INVENTION: EPIITHELINS: NOVEL CYSTEINE-RICH GROWTH
; TITLE OF INVENTION: MODULATING PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,333
FILING DATE: 27-APR-1995

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-431-333-8

Alignment Scores:
Pred. No.: 3.4e-06 Length: 179
Score: 16.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.31% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x US-08-431-333-8 (1-179)

QY 892 TATACCTGCTGCCTACAGTCGGGGCTGGGGCTGCCTGCTGCTTTT 939
|||||

DB 66 TyrThrCysCysArgLeuGlnSerGlyAlaTrpGlyCysCysProPhe 81
|||||

RESULT 19

PCT-US91-02321-8
; Sequence 8, Application PC/TUS9102321
; GENERAL INFORMATION:
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Shoyab, Gregory D.
; TITLE OF INVENTION: EPIITHELINS: NOVEL CYSTEINE-RICH GROWTH
; TITLE OF INVENTION: MODULATING PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02321
FILING DATE: 19910403
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0071A-PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)728-4800
TELEFAX: (206)448-4775

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US91-02321-8

Alignment Scores:
Pred. No.: 3.4e-06 Length: 179
Score: 16.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.31% Indels: 0
DB: 5 Gaps: 0

US-09-824-647-16 (1-2095) x PCT-US91-02321-8 (1-179)

QY 892 TATACCTGCTGCCTACAGTCGGGGCTGGGGCTGCCTGCTGCTTTT 939
|||||

DB 66 TyrThrCysCysArgLeuGlnSerGlyAlaTrpGlyCysCysProPhe 81
|||||

RESULT 20

US-08-991-862-7
; Sequence 7, Application US/08991862
; Patent No. 6309826
; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996.488/P001-A
; CURRENT APPLICATION NUMBER: US/08/991,862
; CURRENT FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/863,862
; EARLIER FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT

ORGANISM: Human granulin
FEATURE: PEPTIDE
NAME/KEY: (1)..
LOCATION: (1)..
OTHER INFORMATION: Internal peptide of human GP88 used to develop neutralizing anti-human GP88 monoclonal antibody.
US-08-991-862-7

Alignment Scores:
Pred. No.: 0.000321 Length: 14
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x US-08-991-862-7 (1-14)

QY 1708 GCACGAGGTTACCAAGTGTTCGCGAGGAGGCCGCGC 1749
|||||
Db 1 AlaArgArgGlyThrLysCysLeuArgargGluAlaProArg 14

RESULT 21
US-08-245-853-2
; Sequence 2, Application US/08245853
; Patent No. 5476839
; GENERAL INFORMATION:
; APPLICANT: SCOTT, RANDY W.
; APPLICANT: GLEICH, GERALD J.
; APPLICANT: WILDE, CRAIG G.
; TITLE OF INVENTION: BASOPHIL GRANULE PROTEINS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/245,853
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: US 07/943,813
; FILING DATE: 11-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BOZICEVIC, KARL
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 24842-20059.20
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-245-853-2

Alignment Scores:
Pred. No.: 0.159 Length: 15
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.59% Indels: 0

DB: 1 Gaps: 0
US-09-824-647-16 (1-2095) x US-08-245-853-2 (1-15)
QY 865 GACATGGAGGTGAGCTGCCAGATGGCTATACC 897
|||||
Db 5 AspMetGluValSerCysProAspGlyTyrThr 15
RESULT 22
US-08-573-675-2
; Sequence 2, Application US/08573675
; Patent No. 5747283
; GENERAL INFORMATION:
; APPLICANT: SCOTT, RANDY W.
; APPLICANT: GLEICH, GERALD J.
; APPLICANT: WILDE, CRAIG G.
; TITLE OF INVENTION: BASOPHIL GRANULE PROTEINS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/573,675
; FILING DATE: 18-DEC-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: US 07/943,813
; FILING DATE: 11-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: GREGG, VALETA
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 06514/013002
; TELEPHONE: (415) 322-5070
; TELEFAX: (415) 854-0875
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-573-675-2
Alignment Scores:
Pred. No.: 0.159 Length: 15
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.59% Indels: 0
DB: 1 Gaps: 0
US-09-824-647-16 (1-2095) x US-08-573-675-2 (1-15)
QY 865 GACATGGAGGTGAGCTGCCAGATGGCTATACC 897
|||||
Db 5 AspMetGluValSerCysProAspGlyTyrThr 15
RESULT 23
5470825-2
; Patent No. 5470825
; APPLICANT: SCOTT, RANDY W.; GLEICH, GERALD J.;
; WILDE, CRAIG G.
; TITLE OF INVENTION: BASOPHIL GRANULE PROTEINS
; NUMBER OF SEQUENCES: 8

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/259,564
;; FILING DATE: 15-JUN-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 551,263
;; FILING DATE: 10-JUL-1990
;; SEQ ID NO:2:
;; LENGTH: 15
5470825-2

Alignment Scores:
Pred. No.: 0.159 Length: 15
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.59% Indels: 0
DB: 6 Gaps: 0

US-09-824-647-16 (1-2095) x 5470825-2 (1-15)

QY 865 GACATGGAGGTGAGCTCCCGAGATGGCTATACC 897
DB 5 AspMetGluValSerCysProAspGlyThr 15

RESULT 24

;; Sequence 732, Application US/09060756
;; Patent No. 6183957
;; GENERAL INFORMATION:

;; APPLICANT: Cole, Stewart
;; APPLICANT: Buchrieser-Brosch, Roland
;; APPLICANT: Gordon, Stephen
;; APPLICANT: Billault, Alain
;; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
;; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
;; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
;; FILE REFERENCE: 3495-0169
;; CURRENT APPLICATION NUMBER: US/09/060,756
;; CURRENT FILING DATE: 1998-04-16
;; NUMBER OF SEQ ID NOS: 743
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 732
;; LENGTH: 29
;; TYPE: PRT
;; ORGANISM: Mycobacterium sp.
US-09-060-756-732

Alignment Scores:
Pred. No.: 71.8 Length: 29
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-060-756-732 (1-29)

QY 1231 GCTGGGGCAGCAGTGGTGGT 1208
DB 6 AlaGlySerAlaGlyGly 13

RESULT 25

;; Sequence 11, Application US/08584031A
;; Patent No. 6030945
;; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.
;; TITLE OF INVENTION: APO-2 LIGAND
;; FILE REFERENCE: 11669.22US03
;; CURRENT APPLICATION NUMBER: US/08/584,031A
;; CURRENT FILING DATE: 1996-01-09
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 11
;; LENGTH: 151
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-08-584-031-11

Alignment Scores:
Pred. No.: 55.3 Length: 151
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 3 Gaps: 0

US-09-824-647-16 (1-2095) x US-08-584-031-11 (1-151)

QY 1734 CAGGAGGCCCGCGCTGGGACGC 1757
DB 32 GlnGlyProAlaLeuGlyArg 39

RESULT 26

;; Sequence 2, Application US/08106507
;; Patent No. 5573924
;; GENERAL INFORMATION:

;; APPLICANT: BECKMANN, M. P.
;; APPLICANT: GOODWIN, RAYMOND G.
;; APPLICANT: GIRI, JUDITH G.
;; APPLICANT: ARMITAGE, RICHARD J.
;; TITLE OF INVENTION: CD27 LIGAND
;; NUMBER OF SEQUENCES: 10
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: IMMUNEX CORPORATION
;; STREET: 51 UNIVERSITY STREET
;; CITY: SEATTLE
;; STATE: WA
;; COUNTRY: USA
;; ZIP: 98101
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/106,507
;; FILING DATE:
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/941,648
;; FILING DATE: 08-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WIGHT, CHRISTOPHER L.
;; REGISTRATION NUMBER: 31,680
;; REFERENCE/DOCKET NUMBER: 2809-A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 206-587-0430
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 193 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-106-507-2

Alignment Scores:
Pred. No.: 53.2 Length: 193
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x US-08-106-507-2 (1-193)

QY 1734 CAGGAGGCCCGCGCTGGGACGC 1757
|||||
Db 76 GlnGlyGlyProAlaLeuGlyArg 83

RESULT 27

US-08-106-507-10
; Sequence 10, Application US/08106507
; Patent No. 5573924
; GENERAL INFORMATION:
; APPLICANT: BECKMANN, M. P.
; APPLICANT: GOODWIN, RAYMOND G.
; APPLICANT: GIRI, JUDITH G.
; APPLICANT: ARMITAGE, RICHARD J.
; TITLE OF INVENTION: CD27 LIGAND
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/106,507
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,648
; FILING DATE: 08-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WIGHT, CHRISTOPHER L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2809-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 216 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-106-507-10

Alignment Scores:
Pred. No.: 52.3 Length: 216
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x US-08-106-507-10 (1-216)

QY 1734 CAGGAGGCCCGCGCTGGGACGC 1757
|||||
Db 99 GlnGlyGlyProAlaLeuGlyArg 106

RESULT 28

US-08-446-922-8
; Sequence 8, Application US/08446922
; Patent No. 5716805
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; APPLICANT: Srinivasan, Subhashini
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,922
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/107,353
; FILING DATE: 08-13-93
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 1003-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 216 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-922-8

Alignment Scores:
Pred. No.: 52.3 Length: 216
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x US-08-446-922-8 (1-216)

QY 1734 CAGGAGGCCCGCGCTGGGACGC 1757
|||||
Db 99 GlnGlyGlyProAlaLeuGlyArg 106

RESULT 29
PCT-US93-10034-8
; Sequence 8, Application PC/TUS9310034
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; APPLICANT: Srinivasan, Subhashini
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10034
; FILING DATE:

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 1003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 216 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-10034-8

Alignment Scores:
Pred. No.: 52.3 Length: 216
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 5 Gaps: 0

US-09-824-647-16 (1-2095) x PCT-US93-10034-8 (1-216)
QY 1734 CAGGGAGGCCCGCGCTGGACGC 1757
Db 99 GlnGlycylProAlaLeuGlyArg 106

RESULT 30
US-08-844-120-3
Sequence 3, Application US/08844120
Patent No. 5858756
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,120
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: PF-0269 US
REFERENCE/DOCKET NUMBER: PF-0269 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 552244
US-08-844-120-3

Alignment Scores:
Pred. No.: 51.8 Length: 230
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x US-08-844-120-3 (1-230)
QY 1686 CTGTCCTGCTGGCTTCGCTGCGC 1709
Db 142 LeuSerCysTrpLeuProLeuArg 149

RESULT 31
US-09-022-940-3
Sequence 3, Application US/09022940
Patent No. 5965423
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,940
FILING DATE: Filed Herewith
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-022-940-3

Alignment Scores:
Pred. No.: 51.8 Length: 230
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-022-940-3 (1-230)
QY 1686 CTGTCCTGCTGGCTTCGCTGCGC 1709
Db 142 LeuSerCysTrpLeuProLeuArg 149

RESULT 32
US-09-022-940-5

;; Sequence 5, Application US/09022940
;; Patent No. 5965423
;; GENERAL INFORMATION:
;; APPLICANT: Hillman, Jennifer L.
;; APPLICANT: Shah, Purvi
;; APPLICANT: Murry, Lynn E.
;; TITLE OF INVENTION: HUMAN LYOPHOSPHOLIPASE
;; NUMBER OF SEQUENCES: 5
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Incyte Pharmaceuticals, Inc.
;; STREET: 3174 Porter Dr.
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94304
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/022,940
;; FILING DATE: Filed Herewith
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Billings, Lucy J.
;; REGISTRATION NUMBER: 36,749
;; REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-845-4166
;; TELEFAX: 650-845-4166
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 230 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: GenBank
;; CLONE: 1552244
;; US-09-022-940-5
Alignment Scores:
Pred. No.: 51.8 Length: 230
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 2 Gaps: 0
US-09-824-647-16 (1-2095) x US-09-022-940-5 (1-230)
QY 1686 CTGCTGCTGGCTTCGCTGGCGC 1709
Db 142 LeuSerCysTrpLeuProLeuArg 149
RESULT 33
US-09-216-001-3
;; Sequence 3, Application US/09216001
;; Patent No. 6004792
;; GENERAL INFORMATION:
;; APPLICANT: Hillman, Jennifer L.
;; APPLICANT: Shah, Purvi
;; APPLICANT: Corley, Neil C.
;; APPLICANT: Murry, Lynn E.
;; TITLE OF INVENTION: NEW HUMAN LYOPHOSPHOLIPASE
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Incyte Pharmaceuticals, Inc.
;; STREET: 3174 Porter Drive
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94304

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/216,001
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/878,862
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Billings, Lucy J.
;; REGISTRATION NUMBER: 36,749
;; REFERENCE/DOCKET NUMBER: PF-0329 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-855-0555
;; TELEFAX: 415-845-4166
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 230 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: GenBank
;; CLONE: 1552244
;; US-09-216-001-3
Alignment Scores:
Pred. No.: 51.8 Length: 230
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 3 Gaps: 0
US-09-824-647-16 (1-2095) x US-09-216-001-3 (1-230)
QY 1686 CTGCTGCTGGCTTCGCTGGCGC 1709
Db 142 LeuSerCysTrpLeuProLeuArg 149
RESULT 34
US-09-216-386-3
;; Sequence 3, Application US/09216386
;; Patent No. 6093561
;; GENERAL INFORMATION:
;; APPLICANT: Hillman, Jennifer L.
;; APPLICANT: Shah, Purvi
;; APPLICANT: Murry, Lynn E.
;; TITLE OF INVENTION: HUMAN LYOPHOSPHOLIPASE
;; NUMBER OF SEQUENCES: 5
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Incyte Pharmaceuticals, Inc.
;; STREET: 3174 Porter Dr.
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94304
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/216,386
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/022,940
;; FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-216-386-3

Alignment Scores:
Pred. No.: 51.8 Length: 230
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 3 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-216-386-3 (1-230)

OY 1686 CTGCTGCTGGCTTCCGCTCGC 1709
Db 142 LeuSerCysTrpLeuProLeuArg 149

RESULT 35
US-09-216-386-5
Sequence 5, Application US/09216386
Patent No. 6093561
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/216,386
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,940
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-216-386-5

Alignment Scores:

Pred. No.: 51.8 Length: 230
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 3 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-216-386-5 (1-230)

OY 1686 CTGCTGCTGGCTTCCGCTCGC 1709
Db 142 LeuSerCysTrpLeuProLeuArg 149

RESULT 36
US-08-878-862-3
Sequence 3, Application US/08878862
Patent No. 6143544
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NEW HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,862
FILING DATE: Herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0329 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1552244
US-08-878-862-3

Alignment Scores:
Pred. No.: 51.8 Length: 230
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x US-08-878-862-3 (1-230)

OY 1686 CTGCTGCTGGCTTCCGCTCGC 1709

Db 142 LeuSerCysTrpLeuProLeuArg 149
RESULT 37
US-09-213-394-3
; Sequence 3, Application US/09213394
; Patent No. 6319701
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL HUMAN LYOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/213,394
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,120
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 552244
US-09-213-394-3
Alignment Scores:
Pred. No.: 51.8 Length: 230
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 4 Gaps: 0
US-09-824-647-16 (1-2095) x US-09-213-394-3 (1-230)
QY 1686 CAGCTCGTGGTTCGCGTGC 1709
Db 142 LeuSerCysTrpLeuProLeuArg 149
RESULT 38
US-09-372-422A-28
; Sequence 28, Application US/09372422A
; Patent No. 6313375
; GENERAL INFORMATION:
; APPLICANT: Rudolf Jung
; APPLICANT: Francois Barrieu
; TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
; FILE REFERENCE: 0919
; CURRENT APPLICATION NUMBER: US/09/372,422A

; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: US 60/098,692
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Zea mays
US-09-372-422A-28
Alignment Scores:
Pred. No.: 50.9 Length: 257
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 4 Gaps: 0
US-09-824-647-16 (1-2095) x US-09-372-422A-28 (1-257)
QY 1362 GCAGCTGGTGGTGCACAGCC 1339
Db 74 AlaAlaGlyValLeuValThrAla 81
RESULT 39
US-09-372-422A-26
; Sequence 26, Application US/09372422A
; Patent No. 6313375
; GENERAL INFORMATION:
; APPLICANT: Rudolf Jung
; APPLICANT: Francois Barrieu
; TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
; FILE REFERENCE: 0919
; CURRENT APPLICATION NUMBER: US/09/372,422A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: US 60/098,692
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Zea mays
US-09-372-422A-26
Alignment Scores:
Pred. No.: 50.4 Length: 272
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 4 Gaps: 0
US-09-824-647-16 (1-2095) x US-09-372-422A-26 (1-272)
QY 1362 GCAGCTGGTGGTGCACAGCC 1339
Db 72 AlaAlaGlyValLeuValThrAla 79
RESULT 40
US-09-282-305-14
; Sequence 14, Application US/09282305
; Patent No. 6287843
; GENERAL INFORMATION:
; APPLICANT: Baldwin, Donald A.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Crane, Virginia C.
; TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
; FILE REFERENCE: 5718-44
; CURRENT APPLICATION NUMBER: US/09/282,305
; CURRENT FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/080,563

; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Zea mays
US-09-282-305-14

Alignment Scores:
Pred. No.: 49.6 Length: 302
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-282-305-14 (1-302)

QY 1822 AGGCTGCAGACTTTCAGTACTG 1799
|||||
Db 209 ArgAlaAlaGluSerSerValLeu 216

RESULT 41

US-09-282-305-12
; Sequence 12, Application US/09282305
; Patent No. 6287843
; GENERAL INFORMATION:
; APPLICANT: Baldwin, Donald A.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Crane, Virginia C.
; TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
; FILE REFERENCE: 5718-44,
; CURRENT APPLICATION NUMBER: US/09/282,305
; CURRENT FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/080,563
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; TYPE: PRT
; ORGANISM: Zea mays
US-09-282-305-12

Alignment Scores:
Pred. No.: 49.5 Length: 305
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-282-305-12 (1-305)

QY 1822 AGGCTGCAGACTTTCAGTACTG 1799
|||||
Db 209 ArgAlaAlaGluSerSerValLeu 216

RESULT 42

US-09-060-756-727
; Sequence 727, Application US/09060756
; Patent No. 6183957
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/060,756

; CURRENT FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 727
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Mycobacterium sp.
US-09-060-756-727

Alignment Scores:
Pred. No.: 49.2 Length: 318
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.16% Indels: 0
DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-060-756-727 (1-318)

QY 1231 GCTGGGCGAGCTGCTGGTGT 1208
|||||
Db 66 AlaGlyGlySerSerAlaGlyGly 73

RESULT 43

US-08-805-118-1
; Sequence 1, Application US/0805118
; Patent No. 5985604
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPENDENT
; TITLE OF INVENTION: PHOSPHATE CO-TRANSPORTER
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/805,118
; FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0221 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAITUT02
; CLONE: 754412
US-08-805-118-1

Alignment Scores:
Pred. No.: 47.4 Length: 401
Score: 8.00 Matches: 8

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.15% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x US-08-805-118-1 (1-401)

QY 380 CCATCCAGTGCCTGATAGTCAGT 403

Db 281 ProSerSerAlaLeuIleValSer 288

RESULT 44

US-09-391-958-1

; Sequence 1, Application US/09391958

; Patent No. 6326207

; GENERAL INFORMATION:

; APPLICANT: Lal, Preeti

; APPLICANT: Bandman, Olga

; TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPENDENT

; TITLE OF INVENTION: PHOSPHATE CO-TRANSPORTER

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: US

; ZIP: 94304

; COMPUTER READABLE FORM:

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/391,958

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/805,118

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0221 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 401 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: BRAITUT02

; CLONE: 754412

US-09-391-958-1

Alignment Scores: 47.4 Length: 401
Pred. No.: 8.00 Matches: 8
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 1.15% Gaps: 0
DB: 4

US-09-824-647-16 (1-2095) x US-09-391-958-1 (1-401)

QY 380 CCATCCAGTGCCTGATAGTCAGT 403

Db 281 ProSerSerAlaLeuIleValSer 288

RESULT 45

US-08-724-394A-11

; Sequence 11, Application US/08724394A

; Patent No. 5872237

; GENERAL INFORMATION:

; APPLICANT: Feder, John N.

; APPLICANT: Krommal, Gregory S.

; APPLICANT: Lauer, Peter M.

; APPLICANT: Ruddy, David A.

; APPLICANT: Thomas, Winston

; APPLICANT: Tsuchihashi, Zenta

; APPLICANT: Welff, Roger K.

; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el

; TITLE OF INVENTION: Sequences and Antibodies Thereto

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/724,394A

; FILING DATE: 01-OCT-1996

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Fitts, Renee A.

; REGISTRATION NUMBER: 35,136

; REFERENCE/DOCKET NUMBER: 017957-000100

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-576-0200

; TELEFAX: 415-576-0300

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 480 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: not relevant

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Region

; LOCATION: 1..480

; OTHER INFORMATION: /note= "NPT4"

US-08-724-394A-11

Alignment Scores: 46.1 Length: 480
Pred. No.: 8.00 Matches: 8
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 1.15% Gaps: 0
DB: 2

US-09-824-647-16 (1-2095) x US-08-724-394A-11 (1-480)

QY 380 CCATCCAGTGCCTGATAGTCAGT 403

Db 360 ProSerSerAlaLeuIleValSer 367

Search completed: July 7, 2003, 15:49:11
Job time : 57 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: July 7, 2003, 15:51:35 ; Search time 91 Seconds
(without alignments)
6135.386 Million cell updates/sec

Title: US-09-824-647-16

Perfect score: 694

Sequence: 1 ccgagcgagaccatggac.....ataaagttgtcactttctt 2095

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 908470 seqs, 133250620 residues

Word size: 1

Total number of hits satisfying chosen parameters: 365718

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL-frame_n2p.model -DEV-xlp
-Q/cygn2.1/USPTO.spool/US09824647/runat.07072003.154758.26607/app_query.fasta_1.2247
-DB-A_Geneseq_101002 -OFMT-fastan -SUFFIX-lim.rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=1 -MATRIX-oligo -TRANS-human40.cdi
-LIST-45 -DOALIGN-200 -THR_SCORE-quality -THR_MIN=1 -ALIGN-45 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=15
-USER-US09824647 -CGEN_1_1_149 -runat.07072003.154758.26607 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	15	2.2	15	14	AAR35077
2	14	2.0	14	20	AAW85481
3	11	1.6	15	13	AAR20737
4	11	1.6	15	15	AAW81665
5	9	1.3	14	14	AAR35078
6	7	1.0	13	21	AAW14948
7	7	1.0	14	20	AAW85479
8	7	1.0	14	22	ABW52180
9	7	1.0	14	22	AAW97797
10	6	0.9	8	15	AAW67120
11	6	0.9	8	16	AAW73224
12	6	0.9	8	16	AAW66383
13	6	0.9	8	19	AAW82944
14	6	0.9	8	20	AAW13573
15	6	0.9	8	20	AAW67665
16	6	0.9	8	23	AAW09998
17	6	0.9	8	23	AAW73544
18	6	0.9	9	16	AAW82184
19	6	0.9	9	19	AAW42528
20	6	0.9	9	20	AAW42208
21	6	0.9	9	20	AAW06031
22	6	0.9	9	20	AAW06039
23	6	0.9	9	20	AAW06025
24	6	0.9	9	20	AAW13578
25	6	0.9	9	20	AAW10533
26	6	0.9	9	22	AAW67189
27	6	0.9	9	22	AAW85641
28	6	0.9	9	22	AAW85642
29	6	0.9	9	22	AAW02357
30	6	0.9	9	22	AAW02355
31	6	0.9	9	22	AAW02360
32	6	0.9	9	22	AAW69921
33	6	0.9	9	23	AAW95803
34	6	0.9	10	10	AAW90829
35	6	0.9	10	16	AAW93340
36	6	0.9	10	18	AAW66370
37	6	0.9	10	18	AAW42311
38	6	0.9	10	19	AAW82826
39	6	0.9	10	20	AAW05999
40	6	0.9	10	20	AAW06009
41	6	0.9	10	20	AAW05997
42	6	0.9	10	20	AAW13579
43	6	0.9	10	20	AAW93872
44	6	0.9	10	20	AAW74014
45	6	0.9	10	22	AAW67204

ALIGNMENTS

RESULT 1
AAR35077
ID AAR35077 standard; protein; 15 AA.
XX
AC AAR35077;
XX
DT 09-AUG-1993 (first entry)
XX
DE N-terminal amino acid sequence of human granulin A.
XX
KW Transforming growth factor e; cell proliferation; mitogen.
XX
OS Homo sapiens.
XX
PN WO9307173-A.
XX
PD 15-APR-1993.
XX
PF 02-OCT-1992; 92WO-US08417.

Tue Jul 8 07:45:06 2003

XX PR 03-OCT-1991; 91US-0770585.
 XX PA (UYGE-) UNIV GEORGIA RES FOUND INC.
 XX PI Halper J, McGraw RA, Farnell PG;
 XX WPI; 1993-134386/16.
 XX DR Transforming growth factor E produced in commercial quantities -
 PT used for wound healing and burns treatment, comprises monomeric
 PT protein which acts as mitogen for fibroblasts
 XX PS Example; Page 49; 60pp; English.
 XX TGFE is a glycoprotein with an Mr of about 25,000. The partial
 CC amino acid sequence of purified bovine TGFE indicated no homology to
 CC other known growth factors. However the N-terminal sequence
 CC exhibits considerable amino acid sequence identity to the deduced N-
 CC terminal amino acid sequence of human granulin A and the N-terminus
 CC of epithelin 1.
 XX SQ Sequence 15 AA;
 Alignment Scores: Length: 15
 Pred. No.: 4.48e-05 Matches: 15
 Score: 15.00
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.16% Indels: 0
 DB: 14 Gaps: 0
 US-09-824-647-16 (1-2095) x AAR35077 (1-15)
 OY 853 GATGTGAATGTGACATGGAGTGAGCTGCCAGATGGCTATACC 897
 DB 1 AspVallylCysaspMetGluValSerCysProaspGlyTyrThr 15
 RESULT 2
 AAR85481
 ID AAR85481 standard; Peptide; 14 AA.
 AC AAR85481;
 XX 15-MAR-1999 (first entry)
 DT Human GP88 autocrine growth factor antigenic peptide A14R.
 DE GP88; granulin; epithelin; human; growth factor; autocrine; tumour;
 KW cancer; viral infection; antagonist; therapy; diagnosis; antigen;
 KW antibody.
 XX Homo sapiens.
 OS WO9852607-A1.
 XX 26-NOV-1998.
 PD 22-MAY-1998; 98WO-US10555.
 PF 16-DEC-1997; 97US-0991862.
 PR 23-MAY-1997; 97US-0863079.
 XX (SERR/) SERRERO G.
 PA Serrero G;
 XX WPI; 1999-045276/04.
 XX Composition containing antagonist of growth factor GP88 - useful for
 XX treating cancer and viral diseases and also for diagnosing disease
 PT from altered GP88 expression.

PS Example 8; Page 45; 86pp; English.

XX This is the amino acid sequence of peptide A14R, comprising amino
 CC acid residues A566-R579 of human GP88 (see AAW85475). GP88 is an 88
 CC kDa glycoprotein autocrine growth factor that is expressed in a
 CC tightly regulated manner in normal cells, is overexpressed and
 CC unregulated in highly tumorigenic cells derived from normal cells,
 CC and which acts as a stringently required growth stimulator for the
 CC tumorigenic cells. A14R was used in an attempt to raise
 CC neutralising antibodies to GP88 (see also AAW85480). Antagonists to
 CC GP88, such as anti-GP88 antibodies, are used to treat diseases
 CC associated with increased expression of GP88, particularly cancer
 CC but also viral infections. Anti-GP88 antibodies can also be used
 CC as diagnostic reagents and to deliver toxins or other compounds to
 CC GP88-expressing cells.

SQ Sequence 14 AA;

Alignment Scores: Length: 14
 Pred. No.: 0.000408 Matches: 14
 Score: 14.00
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0
 DB: 20 Gaps: 0

US-09-824-647-16 (1-2095) x AAW85481 (1-14)

OY 1708 GCACGAGGGTACCAAGTGTTCGCGAGGAGGCCCGGC 1749
 DB 1 AlaArgArgGlyThrLysCysLeuArgGluAlaProArg 14

RESULT 3

AAR20737

ID AAR20737 standard; Protein; 15 AA.

AC AAR20737;

XX 19-MAY-1992 (first entry)

XX BGP N-terminal fraction 11.

XX Basophil granule protein; chronic myelogenous leukemia.

XX Homo sapiens.

XX WO9201000-A.

XX 23-JAN-1992.

XX 09-JUL-1991; 91WO-US04869.

XX 10-JUL-1990; 90US-0551263.

XX (INCY-) INCYTE PHARM INC.

XX Scott RW, Gleich GJ, Wilde GG;

XX WPI; 1992-056828/07.

XX New basophil granule proteins obtd. from cytoplasmic granules -
 CC for diagnosis and treatment of pathologies involving inflammatory
 CC and IgE-mediated responses, infection, hypersensitivity and
 CC leukaemia(s)

XX Claim 2; Page 22; 28pp; English.

XX A patient with a form of chronic myelogenous leukemia underwent two
 CC treatments of cytophoresis from which basophils were recovered.
 CC These were used to search for novel basophil granule proteins (BGP).
 CC The proteins were fractionated. Ca. 25 peaks were identified.
 CC Several fractions were pure enough to allow for the determination of
 CC a single amino acid sequence. The N-terminal sequences of eight

CC such fractions are represented in AAR20736-42 and AAR22455.

XX Sequence 15 AA;

Alignment Scores:

Pred. No.: 0.296 Length: 15
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.59% Indels: 0
DB: 13 Gaps: 0

US-09-824-647-16 (1-2095) x AAR20737 (1-15)

QY 865 GACATGGAGTGGAGTGGCCAGATGGCTATACC 897

Db 5 AspMetGluValSerCysProAspGlyTyrThr 15

RESULT 4

AAR51665

ID AAR51665 standard; protein; 15 AA.

XX AC AAR51665;

XX 24-OCT-1994 (first entry)

XX Basophil granule protein N-terminal sequence.

XX Basophil granule protein; N-terminal sequence;
KW BGP specific antibodies; Antibodies; Leukaemia.

XX Homo sapiens.

XX WO9406829-A.

XX 31-MAR-1994.

XX 10-SEP-1993; 93WO-US08511.

XX 11-SEP-1992; 92US-0943813.

XX (MAYO-) INCYTE PHARM INC.

XX (MAYO-) MAYO FOUNDATION.

XX Gleich GJ, Scott RW, Wilde CG;

XX WPI; 1994-118398/14.

XX New human basophil granule proteins - and related nucleic acid,
PT expression systems, antibodies, etc., for diagnosis and treatment
PT of e.g. inflammation, parasitic infection, leukaemia etc.

XX Claim 2; Page 34; 55pp; English.

XX AAR51665 shows an N-terminal sequence of a basophil granule protein.
CC The BGP can be extracted from human basophil granules by treatment
CC at pH 9.0 or greater. This can be used to generate its corresponding
CC nucleic acid or antibodies. Anti-BGPs are useful for the diagnosis
CC of prepathologic conditions as well as chronic and acute diseases,
CC such as parasitic infection and leukaemia, where there is a change
CC in the amount or distribution of BGPs.

XX Sequence 15 AA;

Alignment Scores:

Pred. No.: 0.296 Length: 15
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.59% Indels: 0
DB: 15 Gaps: 0

US-09-824-647-16 (1-2095) x AAR51665 (1-15)

QY 865 GACATGGAGTGGAGTGGCCAGATGGCTATACC 897

Db 5 AspMetGluValSerCysProAspGlyTyrThr 15

RESULT 5

AAR35078

ID AAR35078 standard; protein; 14 AA.

XX AC AAR35078;

XX 09-AUG-1993 (first entry)

XX N-terminal amino acid sequence of epithelin.

XX Transforming growth factor e; cell proliferation; mitogen.

XX Homo sapiens.

XX WO9307173-A.

XX 15-APR-1993.

XX 02-OCT-1992; 92WO-US08417.

XX 03-OCT-1991; 91US-0770585.

XX (UYGE-) UNIV GEORGIA RES FOUND INC.

XX Halper J, McGraw RA, Parnell PG;

XX WPI; 1993-134386/16.

XX Transforming growth factor E produced in commercial quantities -
PT used for wound healing and burns treatment, comprises monomeric
PT protein which acts as mitogen for fibroblasts

XX Example; Page 49; 60pp; English.

XX TGF α is a glycoprotein with an Mr of about 25,000. The partial
CC amino acid sequence of purified bovine TGF α indicated no homology to
CC other known growth factors. However the N-terminal sequence
CC exhibits considerable amino acid sequence identity to the deduced N-
CC terminal amino acid sequence of human granulin A and the N-terminus
CC of epithelin 1.

XX Sequence 14 AA;

Alignment Scores:

Pred. No.: 24.3 Length: 14
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.30% Indels: 0
DB: 14 Gaps: 0

US-09-824-647-16 (1-2095) x AAR35078 (1-14)

QY 871 GAGCTGAGTGGCCAGATGGCTATACC 897

Db 6 GluValSerCysProAspGlyTyrThr 14

RESULT 6

AAB14948

ID AAB14948 standard; peptide; 13 AA.

XX AC AAB14948;

XX 09-JAN-2001 (first entry)

XX Porphyromonas gingivalis PrTr27 peptide #6.

XX Porphyromonas gingivalis; protective epitope; antiinflammatory; vaccine;

us-09-824-647-16.lim.rag

Tue Jul 8 07:45:06 2003

periodontal disease; periodontitis; immunogen; infection; Prtr27 adhesin.

Porphyrionomas gingivalis.

WO200052041-A1.

08-SEP-2000.

01-MAR-2000; 2000WO-AU00142.

01-MAR-1999; 99AU-0008939.

(UYME) UNIV MELBOURNE.

(VICT-) VICTORIAN DAIRY IND ASSOC.

O'Brien-Simpson NM, Reynolds EC;

WPI; 2000-579275/54.

New compositions comprising at least one peptide with an epitope of arg-specific proteinase associated with Lys-specific proteinase protein complex for treating and preventing periodontitis-associated Porphyrionomas gingivalis

Example 1; Page 21; 62pp; English.

The present sequence is one of twenty overlapping peptides corresponding to the N-terminal 148 residues of the Prtr27 adhesin from Porphyrionomas gingivalis. Antibodies directed towards the Prtr27 adhesin were found to provide protection against periodontitis in a human patient and immunoprotected mice. The peptides were used for epitope mapping of the Prtr27 adhesin. Peptides comprising at least one P. gingivalis epitope are useful in the treatment and prevention of periodontal disease, particularly periodontitis, which is associated with P. gingivalis infection. The peptides are useful as immunogens in vaccine formulations for active immunisation. They may also be used to generate protein-specific and peptide-specific antiserum useful for passive immunisation, and to generate polyclonal or monoclonal antibodies. The peptides and antibodies against the peptides can be used in diagnostic tests to detect P. gingivalis infection. The antibodies can also be used in oral compositions such as toothpaste and mouthwash to neutralise the antigen and prevent disease.

Sequence 13 AA;

Alignment Scores:
Pred. No.: 2e+03 Length: 13
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.02% Indels: 0
DB: 21 Gaps: 0

US-09-824-647-16 (1-2095) x AAB14948 (1-13)

QY 1029 GGGCCCTGTTCACAGGTACC 1009

Db 4 GlyProLeuPheThrGlyThr 10

RESULT 7

AAW85479

ID AAW85479 standard; Peptide; 14 AA.

XX AC AAW85479;

XX 15-MAR-1999 (first entry)

DE Mouse GP88 autocrine growth factor antigenic peptide S14R.

XX GP88; granulatin; epithillin; mouse; growth factor; autocrine; tumour;
KW cancer; viral infection; antagonist; therapy; diagnosis; antigen;
KW antibody.

XX OS Mus sp.

XX PN WO9852607-A1.

XX PD 26-NOV-1998.

XX XX 22-MAY-1998; 98WO-US10555.

XX PR 16-DEC-1997; 97US-0991862.

XX PR 23-MAY-1997; 97US-0863079.

XX (SERR/) SERRERO G.

XX Serrero G;

XX WPI; 1999-045276/04.

Composition containing antagonist of growth factor GP88 - useful for treating cancer and viral diseases and also for diagnosing disease from altered GP88 expression

Example 8; Page 45; 86pp; English.

This is the amino acid sequence of peptide S14R, comprising amino acid residues S562-R575 of murine GP88 (see AAW85474). GP88 is an 88 kDa glycoprotein autocrine growth factor that is expressed in a tightly regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which acts as a stringently required growth-stimulator for the tumorigenic cells. S14R was used to raise neutralising antibodies to GP88. Antagonists to GP88, such as anti-GP88 antibodies, are used to treat diseases associated with increased expression of GP88, particularly cancer but also viral infections. Anti-GP88 antibodies can also be used as diagnostic reagents and to deliver toxins or other compounds to GP88-expressing cells.

XX Sequence 14 AA;

Alignment Scores:
Pred. No.: 1.98e+03 Length: 14
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.01% Indels: 0
DB: 20 Gaps: 0

US-09-824-647-16 (1-2095) x AAW85479 (1-14)

QY 1714 AGGGGTACCAAGTGTTCGCGC 1734

Db 3 ArgGlyThrLysCysLeuArg 9

RESULT 8

ABB52180

ID ABB52180 standard; Peptide; 14 AA.

XX AC ABB52180;

XX 08-FEB-2002 (first entry)

DE Human API-108 tryptic digest peptide #2.

XX Human; neuroprotective; nootropic; gene therapy; vaccine;
KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
XX Expression Reference Protein Isoform; ERPI; proteolysis.

XX Homo sapiens.

XX WO200175454-A2.

XX 11-OCT-2001.

PD

XX PF 03-APR-2001; 2001WO-US10908.
 XX PF 03-APR-2000; 2000US-194504P.
 XX PR 28-NOV-2000; 2000US-253647P.
 XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX PA (PFIZ) PFIZER INC.
 XX PI Durham KL, Friedman DL, Herath HM, Kimmel LH, Parekh RB;
 XX PI Potter DM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;
 XX PI Townsend RR, White F, Williams SA;
 XX DR WPI; 2001-639384/73.
 XX PT Screening for Alzheimer's disease in a mammal, by making
 PT two-dimensional array of a feature whose relative abundance correlates
 PT with disease, and comparing with abundance of the feature in samples of
 PT healthy persons
 XX PS Example; Page 29; 162pp; English.
 XX CC The invention relates to methods for the screening, diagnosis and
 CC prognosis of Alzheimer's disease. The methods involve the detection
 CC of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's
 CC Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid,
 CC serum or plasma. The abundance of the AFs and APIs is then
 CC normalised to an Expression Reference Protein Isoform (ERPI) in
 CC order to determine whether a patient is suffering from, or has
 CC a predisposition to, Alzheimer's disease. The relative abundance of
 CC the AFs and APIs correlates with the severity of Alzheimer's disease.
 CC The present sequence is a peptide produced from an API by proteolysis.
 XX SQ Sequence 14 AA;
 Alignment Scores:
 Pred. No.: 1.98e+03 Length: 14
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.01% Indels: 0
 DB: 22 Gaps: 0
 US-09-824-647-16 (1-2095) x ABB52180 (1-14)
 QY 1009 GGTACTGTGACAGGGGCC 1029
 DB 1 GlyThrCysGluGlnGlyPro 7
 RESULT 9
 AAM97797
 ID AAM97797 standard; Peptide; 14 AA.
 XX AC AAM97797;
 XX DT 24-JAN-2002 (first entry)
 XX DE Human peptide #1072 encoded by a SNP oligonucleotide.
 XX KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.
 XX OS Homo sapiens.
 XX PN WO200147944-A2.
 XX PD 05-JUL-2001.

XX PF 28-DEC-2000; 2000WO-US35498.
 XX PR 28-DEC-1999; 99US-0173419.
 XX PR 27-DEC-2000; 2000US-0173419.
 XX PA (CURA-) CURAGEN CORP.
 XX PI Shimkets RA, Leach M;
 XX DR WPI; 2001-465210/50.
 XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections
 XX PS Disclosure; Page 3902; 4143pp; English.
 XX CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinesins, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.
 CC The oligonucleotides and the peptides encoded by them may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the proteins listed above. Disorders that may
 CC be prevented, diagnosed and/or treated include multifactorial diseases
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
 CC system and an infection of pathogenic organisms.
 XX SQ Sequence 14 AA;
 Alignment Scores:
 Pred. No.: 1.98e+03 Length: 14
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.01% Indels: 0
 DB: 22 Gaps: 0
 US-09-824-647-16 (1-2095) x AAM97797 (1-14)
 QY 264 CCCTTCCAGAGCCGTGGC 284
 DB 2 ProLeuProArgGlyArgGly 8
 RESULT 10
 AAR67120
 ID AAR67120 standard; peptide; 8 AA.
 XX AC AAR67120;
 XX DT 30-JUN-1995 (first entry)
 XX DE PGF inhibitor (PGF-3), contg. proline brackets.
 XX KW platelet derived growth factor; PDGF; smooth muscle;
 KW mimic; interaction site; constrained conformation; inhibitor.
 XX OS Synthetic.
 XX PN WO9425482-A.
 XX PD 10-NOV-1994.
 XX PF 21-APR-1994; 94WO-US04294.
 XX PR 23-APR-1993; 93US-0051741.

Tue Jul 8 07:45:06 2003

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PR 29-OCT-1993; 93US-0143364.
XX (EVAN/) EVANS H J.
PA (KINI/) KINI R M.
XX EVANS HJ, Kini RM;
PI WPI; 1994-358186/44.
DR
XX Peptide homologue or analogue with constrained conformation - has
PT proline residues flanking the interaction site to impart greater,
PT or more stable, biological activity
XX
XX Example 3; Page 39; 57pp; English.
XX
XX AAR67118-20 are platelet derived growth factor (PDGF) inhibitors and
CC are deriv. from PDGF peptides that contain proline or proline/cysteine
CC brackets. These peptides contain one or more interaction sites of
CC interest. The dose is 5-5000 micrograms. The peptides interact
CC with specific receptors and inhibit the migration of macrophages,
CC and thus inhibits the pro-inflammatory effects of the interleukin. The
CC data collected demonstrates that interaction sites possess activity when
CC present in a polypeptide that differs from the native form. Inclusion of
CC conformation-constraining moieties can have desirable effects on an
CC interaction site. (Also see AAR67011-117 and AAR67121-52 for analogues
CC of other biologically active peptides contg. an interaction site flanked
CC by conformation constraining gps., eg. RGD peptides.)
XX
XX Sequence 8 AA;

Alignment Scores:
Pred. No.: 3.31e+07 Length: 8
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 15 Gaps: 0

US-09-824-647-16 (1-2095) x AAR67120 (1-8)
QY 270 CCCAGAGCCGTCGATG 287
DB 1 PROARGLYARGGLYMet 6

RESULT 11
AAR73224
ID AAR73224 standard; Peptide; 8 AA.
XX
XX AAR73224;
AC
XX 07-DEC-1995 (first entry)
DT
XX Human TSH receptor (residues 47-54).
DE
XX thyroid stimulating hormone receptor; TSH; human; Homo sapiens;
KW antibody; affinity; detection.
KW
XX Synthetic.
XX
XX JP07089991-A.
PN
XX 04-APR-1995.
PD
XX 28-SEP-1993; 93JP-0240853.
PF
XX 28-SEP-1993; 93JP-0240853.
PR
XX (MTP ) MITSUBISHI PETROCHEMICAL CO LTD.
PA
XX WPI; 1995-167251/22.
DR
XX Novel polypeptide(s) having affinity for the human TSH receptor
PT antibody - used in detection of the TSH antibody.
PT

XX Example 1; Page 11; 54pp; Japanese.
XX
XX Peptides with affinity to human TSH (thyroid stimulating hormone)
CC receptor antibody are used for detection of the antibody. (See also
CC AAR73201-592).
XX
XX Sequence 8 AA;
SQ

Alignment Scores:
Pred. No.: 3.31e+07 Length: 8
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 16 Gaps: 0

US-09-824-647-16 (1-2095) x AAR73224 (1-8)
QY 1517 CCCAGCGTCGACCTTCC 1534
DB 2 ProSerLeuProSer 7

RESULT 12
AAR66383
ID AAR66383 standard; peptide; 8 AA.
XX
XX AAR66383;
AC
XX 27-JUN-1995 (first entry)
DT
XX Chlamydial VDI epitope.
DE
XX Chlamydial epitope; variable domain; MOMP;
KW major outer membrane protein; picorna virus; vaccine; PVI;
KW diagnostic; therapeutic; poliovirus; capsid protein.
KW
XX Chlamydia trachomatis serovar A.
XX
XX WO9426900-A.
PN
XX 24-NOV-1994.
PD
XX 12-MAY-1994; 94WO-CA00262.
PF
XX 13-MAY-1993; 93US-0060978.
PR
XX (CONN-) CONNAUGHT LAB LTD.
PA
XX Caldwell HD, Klein MH, Murdin AD, Oomen RP;
PI WPI; 1995-006796/01.
DR
XX New hybrid picornaviruses expressing chlamydial epitopes - used
PT to develop prods. for vaccination, diagnosis, treatment of
PT chlamydial infections and prodn. of immunological reagents
PT
XX Disclosure; Page 19; 99pp; English.
XX
XX To obtain a poliovirus-1 (PVI)/chlamydial hybrid, the PVI
CC Mahoney cDNA clone p7XLD was modified to encode epitopes from
CC C. trachomatis ser. A MOMP VDI. The VDI sequence was not
CC restricted to the known epitope given in AAR66386, or to the
CC sequence given in AAR66383 (expressed in previously described
CC hybrids), but instead included adjacent sequences from VDI.
XX
XX Sequence 8 AA;
SQ

Alignment Scores:
Pred. No.: 3.31e+07 Length: 8
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

```


Query Match: 0.86% Indels: 0
DB: 16 Gaps: 0

US-09-824-647-16 (1-2095) x AAW6383 (1-8)

QY 1279 GTGCTGGACTGGAGAG 1296

DB 2 ValAlaGlyLeuGlulys 7

RESULT 13

AAW82944

ID AAW82944 standard; peptide; 8 AA.

XX AC AAW82944;

XX DT 04-FEB-1999 (first entry)

XX XX Oestrogen receptor activity inhibiting peptide #1.
DE Human; oestrogen receptor activity inhibitor; anti-oestrogen; diagnosis;
KW breast cancer; estrogen; tumour; phosphotyrosyl peptide;
KW malonyltirosyl peptide; steroid receptor co-activator-1.
XX Synthetic.
OS Homo sapiens.
XX WO9846250-A1.
XX 22-OCT-1998.
XX 14-APR-1998; 98WO-US07711.
XX 14-APR-1997; 97US-0043545.
XX (REGC) UNIV CALIFORNIA.
XX Pietras RJ;
XX WPI; 1998-594522/50.

PT New anti-oestrogen peptide compositions - comprise sequences based
PT on oestrogen receptor and steroid receptor co-activator-1 sequences,
PT used for treating cancers
XX Claim 1; Page 157; 182pp; English.

XX The present invention describes a composition comprising an isolated
XX oestrogen receptor activity inhibiting (anti-oestrogen) peptide. The
XX peptides used in the composition comprise sequences of human oestrogen
XX receptor (OR) surrounding Tyr537 and steroid receptor co-activator-1
XX (SRC-1). The peptide compositions, nucleic acids and vectors of the
XX present invention can reduce OR activity in a cell, reduced OR
XX polypeptide dimerisation in a cell and reduce the binding of SRC-1
XX polypeptide to an OR polypeptide dimer in a cell. They can be used for
XX killing cancer cells and treating cancers, particularly breast cancer.
XX The present sequence represents a specifically claimed anti-oestrogen
XX peptide.

XX SQ Sequence 8 AA;

Alignment Scores:

Pred. No.: 3.31e+07 Length: 8

Score: 6.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 0.86% Indels: 0

DB: 19 Gaps: 0

US-09-824-647-16 (1-2095) x AAW82944 (1-8)

QY 1131 CTCCTCCGATACCTGCTG 1148

DB 1 LeuLeuArgTyrLeuLeu 6

RESULT 14

AAV13573

ID AAV13573 standard; peptide; 8 AA.

XX AC AAV13573;

XX DT 30-JUL-1999 (first entry)

XX DE Peptide sensor TUK-1390.

XX XX Nuclear hormone receptor; sensor peptide; receptor binding; screening;
KW modulator.
KW Synthetic.
XX OS
XX PN WO9927365-A1.
XX PD 03-JUN-1999.
XX PF 20-NOV-1998; 98WO-US24969.
XX PR 30-SEP-1998; 98US-0163713.
XX PR 21-NOV-1997; 97US-0975614.
XX PA (TULA-) TULARIK INC.
XX PI Baeuerle P, Beckmann H, Chen J, Lustig K, Shan B;
XX WPI; 1999-347794/29.
XX Nuclear hormone receptor drug screens
XX Claim 7; Page 17; 29pp; English.

XX The invention provides methods for screening of modulators of nuclear
XX hormone receptor function. The methods use a sensor peptide covalently
XX coupled to a detectable label, that provides direct, in vitro ligand-
XX dependent binding to a nuclear hormone receptor. Panels of predetermined
XX or randomized candidate sensors are readily screened for receptor
XX binding. The methods and compositions provide for efficient screening of
XX modulators of nuclear hormone receptor function, without the use of
XX cell- or gel-based steps. The methods are amenable to automates, for
XX cost-effective high throughput screening of chemical libraries for
XX bioactive compounds. To ensure specificity and optimize binding, the
XX sensor is generally present at sub-micromolar concentration and the
XX binding reaction occurs in solution. The sensor peptide obviates the need
XX to include a natural coactivator protein of the receptor in the mixture.
XX Sequences AAV13571-587 represent examples of sensor peptides that can be
XX used in the method of the invention.

XX SQ Sequence 8 AA;

Alignment Scores:

Pred. No.: 3.31e+07 Length: 8

Score: 6.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 0.86% Indels: 0

DB: 20 Gaps: 0

US-09-824-647-16 (1-2095) x AAV13573 (1-8)

QY 1131 CTCCTCCGATACCTGCTG 1148

DB 1 LeuLeuArgTyrLeuLeu 6

RESULT 15

AAW67665

ID AAW67665 standard; peptide; 8 AA.

XX AC AAW67665;

XX XX

us-09-824-647-16.lim.rag

Tue Jul 8 07:45:06 2003

50S; L17; protein sequencing; protein quantitation.

Escherichia coli.
Key Location/Qualifiers
Modified-site 1
FT /note= "H4/D4 nicotinylated"

WO200174842-A1.

11-OCT-2001.

03-APR-2001; 2001WO-AU00366.

03-APR-2000; 2000AU-0006643.

(PROT-) PROTEOME SYSTEMS LTD.

James P;

WPI; 2002-017393/02.

Method for labeling proteins, useful for identification, particularly in expression analysis, by blocking lysine sidechains, proteolysis and N-terminal labeling of peptide fragments

Disclosure; Fig 2A; 27pp; English.

This sequence represents a peptide fragment of the E.Coli 50S ribosomal subunit L17 identified and characterised using a novel method of the invention. The invention comprises a method for labeling a protein by protecting epsilon-amino groups of lys, cleaving the protein to produce a mixture of peptides and treating these with a labeling agent that binds to the N-terminal amino acid. The method is used for identifying proteins, e.g. for analysis of proteins expressed by cells in different expression states. The method makes possible relative protein quantitation in one- or two-dimensional gel separations, even when separation is only partial, and facilitates de novo sequencing and automated interpretation of mass spectra. Protection of lys sidechains ensures specific labeling of the N-termini, increases the intensity of b-ions (permitting full-length sequence coverage for peptides of m/z over 1000) and allows differentiation between lys and Glu. The use of different isotopic labels allows different proteins in the same gel spot to be quantified.

Sequence 8 AA;

Alignment Scores:
Pred. No.: 3.31e+07 Length: 8
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.87% Indels: 0
DB: 23 Gaps: 0

US-09-824-647-16 (1-2095) x AAU09998 (1-8)

QY 839 GCAGCGAGCTTAGTCAGG 822

DB 3 AlaGlySerLeuValarg 8

RESULT 17

AAU73544

ID AAU73544 standard; Peptide; 8 AA.

AC AAU73544;

XX 12-MAR-2002 (first entry)

DT Vascular endothelial growth factor receptor-2 peptide modulator #121.

DE Vascular endothelial growth factor receptor-2; VEGFR-2;

KW VEGF modulator; psoriasis; rheumatoid arthritis; retinopathy;

XX

16-MAR-1999 (first entry)

LXXLL signature motif #5 from protein SRC1a DNA binding domain.

Nuclear protein; signature motif; receptor protein; inflammation; cancer; interaction; inhibitor; inhibition; transcription factor; ligand.

Homo sapiens.

WO9849561-A1.

05-NOV-1998.

28-APR-1998; 98WO-GB01238.

30-APR-1997; 97GB-0008676.

(IMCR) IMPERIAL CANCER RES TECHNOLOGY.

Heery DM, Parker MG;

WPI; 1999-034672/03.

Identification of inhibitors of nuclear protein/nuclear receptor interaction - useful for, e.g. treatment of disease mediated through the interaction such as inflammation and cancer

Example 1; Fig 1A; 60pp; English.

This sequence represents an LXXLL nuclear protein signature motif found in the DNA binding domain (DBD) of the SRC1a protein. This peptide corresponds to amino acids 748-755 of SRC1a-DBD. The invention relates to the identification of inhibitor compounds capable of reducing the interaction between a region on a nuclear protein (R1) and a region on a nuclear receptor (R2), where: (i) R1 is a signature motif; (ii) R2 is the region capable of interacting with the nuclear protein by binding the signature motif; (iii) the nuclear protein is a bridging factor and a responsible for interaction between a liganded nuclear receptor and a transcription initiation complex involved in gene expression regulation; (iv) the nuclear receptor is a transcription factor; (v) the signature motif is a short amino acid sequence which is the key structural element of a nuclear protein which binds to a liganded nuclear receptor during activation or repression of target genes. The inhibitors are expected to be useful in the treatment of any disease mediated through any interaction between a signature motif on a nuclear protein and a nuclear receptor, for example inflammation and cancer.

Sequence 8 AA;

Alignment Scores:
Pred. No.: 3.31e+07 Length: 8
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 20 Gaps: 0

US-09-824-647-16 (1-2095) x AAU67665 (1-8)

QY 1131 CTCCTCCGATACCTGCTG 1148

DB 1 LeuLeuArgTyrLeuLeu 6

RESULT 16

AAU09998

ID AAU09998 standard; peptide; 8 AA.

XX AAU09998;

XX 12-MAR-2002 (first entry)

DE E.Coli 50S ribosomal subunit L17 peptide.

XX

KW cancer; cytostatic; ophthalmological; neovascularisation;
 KW angiogenesis; coronary artery disease.

OS Synthetic.

PN WO200183693-A2.

XX 08-NOV-2001.

XX 27-APR-2001; 2001WO-US13598.

XX 28-APR-2000; 2000US-0561470.

XX (GLAXO) GLAXO GROUP LTD.

XX Schatz PJ, Chen M, Piplani S, Mozsgai CA, Balu P;

XX WPI; 2002-075158/10.

XX Novel compounds having affinity for vascular endothelial growth factor
 PT receptor-2 useful for treating cancer, retinopathy, rheumatoid
 PT arthritis, psoriasis and as angiogenesis imaging agents

PS Claim 19; Page 40; 101pp; English.

XX The invention describes a compound having affinity for vascular
 CC endothelial growth factor receptor-2 (VEGFR-2) and which acts as
 CC modulator of VEGF function. The compound is useful for: treating a
 CC patient suffering from psoriasis, rheumatoid arthritis, retinopathy and
 CC cancer; for imaging and assessing neovascularisation during angiogenesis;
 CC for detecting VEGFR-2 receptor or related receptor on living cells, as a
 CC calibration standard for quantitating the activities of candidate VEGFR-2
 CC antagonists in a variety of functional assays; as probes for affinity
 CC screening; as blocking reagent in random peptide screening i.e. in
 CC screening for new families of VEGFR-2 peptide ligands; in the
 CC co-crystallisation with VEGFR-2; in inhibiting or decreasing the
 CC proliferation and growth of vascular endothelial cell growth
 CC factor-dependent cell lines e.g. human umbilical vein endothelial cells
 CC (HUVEC) and other research and diagnostic applications where VEGFR-2 is
 CC antagonised. Agonists are useful for the treatment of diseases such as
 CC coronary artery disease. This sequence is a peptide modulator of the
 CC vascular endothelial growth factor receptor-2 (VEGFR-2) based on the
 CC generic peptide sequence AAS73422, described in the method of the
 CC invention.

XX Sequence 8 AA;

Alignment Scores:
 Pred. No.: 3.31e+07 Length: 8
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.87% Indels: 0
 DB: 23 Gaps: 0

US-09-824-647-16 (1-2095) x AAU73544 (1-8)

QY 1832 TGGGGTCCCGAGGCTGC 1815

DB 2 TrpGlyProGluGlyCys 7

RESULT 18

AA82184

ID AAR82184 standard; peptide; 9 AA.

XX AAR82184;

XX 25-MAR-1996 (first entry)

XX Melanoma-specific mutant immunogen epitope 9mer peptide.

KW Melanoma; immunogen; epitope; homologue; vaccine; immunotherapy;
 KW cytotoxic T cell; lymphocyte; HLA-A2.

XX Homo sapiens.

XX WO9522561-A2.

XX 24-AUG-1995.

XX 16-FEB-1995; 95WO-US01991.

XX 29-APR-1994; 94US-0234784.

XX 16-FEB-1994; 94US-0197399.

XX (UYVI-) UNIV VIRGINIA PATENT FOUND.

XX Cox AL, Engelhard VH, Hunt DF, Shabanowitz J, Slingluff CL;

XX WPI; 1995-302688/39.

XX Melanoma-specific immunogen comprises epitope(s) homologous with
 PT pMel.17 - are highly potent stimulators of HLA-A2+CTL's useful in
 PT adoptive immuno-therapy

XX Example 8; Page 52; 148pp; English.

XX A melanoma-specific immunogen homologous with pMel-17 comprises one
 CC or more CTL (cytotoxic T lymphocyte) epitopes from the group AAR82098-
 CC AAR82194 capable of eliciting a CTL response. The epitopes AAR82098-
 CC AAR82194 are of particular interest. The immunogen can be used for
 CC partial protection in mammals against melanoma peptides which are
 CC homologous with pMel-17 are highly potent stimulators of HLA-A2+
 CC CTLs in several cell lines and can be used in immunotherapy or
 CC incorporated into immunogenic conjugates as vaccines.

XX Sequence 9 AA;

Alignment Scores:
 Pred. No.: 2.94e+07 Length: 9
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.86% Indels: 0
 DB: 16 Gaps: 0

US-09-824-647-16 (1-2095) x AAR82184 (1-9)

QY 1982 TTACAGCTGCCATCC 1999

DB 2 LeuGlnAlaAlaIlePro 7

RESULT 19

AAW42528

ID AAW42528 standard; peptide; 9 AA.

XX AAW42528;

XX 22-JUN-1998 (first entry)

XX Melan A/MART epitope (residues 27-35) analogue #5.

XX Metastatic melanoma; peptide analogue; vaccine; cancer; diagnosis;
 KW antigen; CTL; immunogenic; viral disease; gp 100; Melan A/MART-1.

XX Synthetic.

OS Homo sapiens.

XX WO9802538-A1.

XX 22-JAN-1998.

XX 08-JUL-1997; 97WO-EP03712.

XX 11-JUL-1996; 96EP-0201945.

predetermined nuclear receptor having ligand binding domain (LBD)

Example 1; Fig 1; 67pp; English.

The present invention describes the use of a ligand binding domain (LBD) transcription factor (TRX) fusion protein in methods for identifying agonists or antagonists for ligand-induced activation of a predetermined nuclear receptor having a LBD. Also described are: (1) a positive hybrid nuclear receptor signal transduction system, comprising an intact eukaryotic host cell; (2) a nuclear receptor reporter host cell; (3) a multiplexed format comprising a reverse hybrid reporter host cell; (4) identifying a candidate pharmaceutical agent from a library of test agents; (5) a assay for identifying nuclear receptor ligands; and (6) an agonist ligand of a polypeptide comprising a binding amino acid sequence that is non-naturally occurring in a nuclear protein, and predetermined to bind to a nuclear receptor, typically by interaction with a binding interface of a nuclear receptor at which naturally occurring coactivators and/or corepressors bind; and (6) an agonist ligand of a nuclear receptor identified using above methods. The new methods are useful for identifying agonists or antagonists for ligand-induced activation of a predetermined nuclear receptor having a LBD. The present sequence represents a coactivator leucine charged domain peptide, used in an example from the present invention.

Sequence 9 AA;

Alignment Scores:
Pred. No.: 2.94e+07
Score: 6.00
Length: 9
Matches: 6
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 0.86%
Indels: 0
DB: 20
Gaps: 0

US-09-824-647-16 (1-2095) x AAY42208 (1-9)

Oy 1131 CTCCTCCGATACCTGCTG 1148

Db 1 LeuLeuArgTyrLeuLeu 6

RESULT 21

RAY06031

ID AAY06031 standard; Peptide; 9 AA.

AC AAY06031;

DT 16-AUG-1999 (first entry)

DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.

OS Homo sapiens.

PN WO9918206-A2.

PD 15-APR-1999.

PF 21-SEP-1998; 98WO-US19609.

PR 08-OCT-1997; 97US-0061428.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Rosenberg SA, Wang RF;

XX WPI; 1999-277270/23.

PA (ALKU) AKZO NOBEL NV.

PI Adema GJ, Figdor CG;

DR WPI; 1998-110586/10.

PT Melanoma associated peptide analogues - useful in vaccines against melanoma

Example 1; Page 28; 47pp; English.

This sequence is shown in the specification. The invention relates to peptides, which are immunogenic with lymphocytes directed against metastatic melanomas. They are characterised in that they comprise at least a part of the following sequence, where the amino acid at position 2 or 8 is substituted: Lys-Thr-Trp-Gly-Gln-Tyr-Trp-Gln-Val. Vaccines comprising the peptide, or an antigen presenting cell preloaded with the peptide or antibody as above, are useful for cancer, particularly melanoma, treatment. The peptides can also be used to generate antigen reactive tumour infiltrating lymphocytes, which can also be used in vaccines. The peptides can be exploited to elicit native epitope-reactive CTL. Usage of the peptides with improved immunogenicity may contribute to the development of CTL-epitope based vaccines in viral disease and cancer.

Sequence 9 AA;

Alignment Scores:
Pred. No.: 2.94e+07
Score: 6.00
Length: 9
Matches: 6
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 0.87%
Indels: 0
DB: 19
Gaps: 0

US-09-824-647-16 (1-2095) x AAY42528 (1-9)

Oy 903 GCAGAGGTATAGGCATC 886

Db 1 AlaAlaGlyIleAlaIle 6

RESULT 20

RAY42208

ID AAY42208 standard; peptide; 9 AA.

AC AAY42208;

DT 16-DEC-1999 (first entry)

DE Coactivator leucine charged domain peptide #3.

XX Oestrogen receptor beta; ER-beta; MBP; binding; detection;
KW ligand-dependent nuclear receptor; coactivator interaction;
KW hybrid system; corepressor; ligand binding domain; LBD.

OS Synthetic.

PN WO9950664-A1.

PD 07-OCT-1999.

PF 01-APR-1999; 99WO-US07168.

PR 01-APR-1998; 98US-0053611.

XX (GLAXO) GLAXO GROUP LTD.

XX Northrop JP, Hart CP, Schatz PJ;

XX WPI; 1999-591374/50.

PT Identifying agonists or antagonists for ligand-induced activation of

XX Cancer antigen NY ESO1/CAG-3
 XX
 XX
 XX Example 10; Page 43; 88pp; English.
 XX
 CC This peptide was identified as an HLA peptide motif following a
 CC screen for epitopes from the coding region of human ESO-1/CAG-3
 CC ORF1 (see AAX58599). 30 Epitopes (see AAY06018-47) were identified.
 CC The present peptide (ranked 14) corresponds to amino acid residues
 CC 153-160 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
 CC tumour antigen capable of eliciting an antigen specific immune
 CC response by T cells. Cancer peptides (see AAY05967-87) derived from
 CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
 CC vaccines. A claimed method of preventing or inhibiting cancer
 CC involves administering a cancer peptide, with or without an HLA
 CC molecule. The cancer peptides form part of, or are derived
 CC from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
 CC cancer, cervical cancer, bladder cancer, kidney cancer and
 CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
 CC thyroid cancers.
 XX
 XX Sequence 9 AA;
 SQ
 Alignment Scores:
 Pred. No.: 2.94e+07 Length: 9
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.86% Indels: 0
 DB: 20 Gaps: 0
 US-09-824-647-16 (1-2095) x AAY06031 (1-9)
 QY 1119 CAGCAGCTGCTCCCTCCTC 1136
 Db |||||
 2 GlnGlnLeuSerLeuLeu 7
 RESULT 22
 AAY06039
 ID AAY06039 standard; Peptide; 9 AA.
 XX
 AC AAY06039;
 XX
 XX 16-AUG-1999 (first entry)
 XX Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
 XX
 KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine; human leukocyte antigen; HLA.
 XX
 OS Homo sapiens.
 XX
 XX WO9918206-A2.
 XX
 XX 15-APR-1999.
 XX
 XX 21-SEP-1998; 98WO-US19609.
 XX
 XX 08-OCT-1997; 97US-0061428.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Rosenberg SA, Wang RF;
 XX WPI; 1999-277270/23.
 XX
 XX Cancer antigen NY ESO1/CAG-3
 XX
 XX Example 10; Page 43; 88pp; English.

XX
 PS Example 10; Page 43; 88pp; English.
 XX
 CC This peptide was identified as an HLA peptide motif following a
 CC screen for epitopes from the coding region of human ESO-1/CAG-3
 CC ORF1 (see AAX58599). 30 Epitopes (see AAY06018-47) were identified.
 CC The present peptide (ranked 22) corresponds to amino acid residues
 CC 152-160 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
 CC tumour antigen capable of eliciting an antigen specific immune
 CC response by T cells. Cancer peptides (see AAY05967-87) derived from
 CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
 CC vaccines. A claimed method of preventing or inhibiting cancer
 CC involves administering a cancer peptide, with or without an HLA
 CC molecule. The cancer peptides form part of, or are derived
 CC from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
 CC cancer, cervical cancer, bladder cancer, kidney cancer and
 CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
 CC thyroid cancers.
 XX
 XX Sequence 9 AA;
 SQ
 Alignment Scores:
 Pred. No.: 2.94e+07 Length: 9
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.86% Indels: 0
 DB: 20 Gaps: 0
 US-09-824-647-16 (1-2095) x AAY06039 (1-9)
 QY 1119 CAGCAGCTGCTCCCTCCTC 1136
 Db |||||
 3 GlnGlnLeuSerLeuLeu 8
 RESULT 23
 AAY06025
 ID AAY06025 standard; Peptide; 9 AA.
 XX
 AC AAY06025;
 XX
 XX 16-AUG-1999 (first entry)
 XX Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
 XX
 KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine; human leukocyte antigen; HLA.
 XX
 OS Homo sapiens.
 XX
 XX WO9918206-A2.
 XX
 XX 15-APR-1999.
 XX
 XX 21-SEP-1998; 98WO-US19609.
 XX
 XX 08-OCT-1997; 97US-0061428.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Rosenberg SA, Wang RF;
 XX WPI; 1999-277270/23.
 XX
 XX Cancer antigen NY ESO1/CAG-3
 XX
 XX Example 10; Page 43; 88pp; English.

XX This peptide was identified as an HLA peptide motif following a
 CC screen for epitopes from the coding region of human ESO-1/CAG-3
 CC ORP1 (see AAX58599). 30 Epitopes (see AAY06018-47) were identified.
 CC The present peptide (ranked 8) corresponds to amino acid residues
 CC 154-162 of CAG-1 ORP1 (see AAY05965). CAG-1 is a new and potent
 CC tumour antigen capable of eliciting an antigen specific immune
 CC response by T cells. Cancer peptides (see AAY05967-87) derived from
 CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
 CC vaccines. A claimed method of preventing or inhibiting cancer
 CC involves administering a cancer peptide, with or without an HLA
 CC molecule. The cancer peptides form part of, or are derived
 CC from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
 CC cancer, cervical cancer, bladder cancer, kidney cancer and
 CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
 CC thyroid cancers.

XX SQ Sequence 9 AA;

Alignment Scores:

Pred. No.:	2.94e+07	Length:	9
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	0.86%	Indels:	0
DB:	20	Gaps:	0

US-09-824-647-16 (1-2095) x AAY06025 (1-9)

QY 1119 CAGCAGCTGCTCCCTCCTC 1136
 |||||
 DB 1 GlGlnLeuSerLeuLeu 6

RESULT 24
 AAY13578
 ID AAY13578 standard; peptide; 9 AA.
 AC AAY13578;
 XX 30-JUL-1999 (first entry)
 DT Peptide sensor TUK-1472.
 DE Nuclear hormone receptor; sensor peptide; receptor binding; screening;
 KW modulator.
 XX Synthetic.
 OS WO9927365-A1.
 PN 03-JUN-1999.
 PD 20-NOV-1998; 98WO-US24969.
 PF 30-SEP-1998; 98US-0163713.
 PR 21-NOV-1997; 97US-0975614.
 XX (TULA-) TULARIK INC.
 PA Baeuerle P, Beckmann H, Chen J, Lustig K, Shan B;
 PI WPI; 1999-347794/29.
 DR Nuclear hormone receptor drug screens
 XX Claim 7; Page 18; 29pp; English.
 PS The invention provides methods for screening of modulators of nuclear
 CC hormone receptor function. The methods use a sensor peptide covalently
 CC coupled to a detectable label, that provides direct, in vitro ligand-
 CC dependent binding to a nuclear hormone receptor. Panels of predetermined
 CC or randomized candidate sensors are readily screened for receptor

CC binding. The methods and compositions provide for efficient screening of
 CC modulators of nuclear hormone receptor function, without the use of
 CC cell- or gel-based steps. The methods are amenable to automated,
 CC cost-effective high throughput screening of chemical libraries for
 CC bioactive compounds. To ensure specificity and optimize binding, the
 CC sensor is generally present at sub-micromolar concentration and the
 CC binding reaction occurs in solution. The sensor peptide obviates the need
 CC to include a natural coactivator protein of the receptor in the mixture.
 CC Sequences AAY13571-587 represent examples of sensor peptides that can be
 CC used in the method of the invention.

XX SQ Sequence 9 AA;

Alignment Scores:

Pred. No.:	2.94e+07	Length:	9
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	0.86%	Indels:	0
DB:	20	Gaps:	0

US-09-824-647-16 (1-2095) x AAY13578 (1-9)

QY 1131 CTCCTCCGATACCTGCTG 1148
 |||||
 DB 1 LeuLeuArgTyrLeuLeu 6

RESULT 25
 AAY10533
 ID AAY10533 standard; Peptide; 9 AA.
 AC AAY10533;
 XX 12-MAY-1999 (first entry)
 DT HLA Class I motif peptide SEQ ID NO:463.

DE Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;
 XX immunisation; tumour; infectious disease; immunotherapy; cancer;
 KW malignant melanoma; viral disease; hepatitis; AIDS.
 XX Synthetic.
 OS Homo sapiens.
 OS WO9902183-A2.
 PN 21-JAN-1999.
 PD 10-JUL-1998; 98WO-US14289.
 PF 10-DEC-1997; 97US-0988320.
 PR 10-JUL-1997; 97CA-2209815.

XX (CTLI-) CTL IMMUNOTHERAPIES CORP.

XX Kuendig TM, Simard JJJ;

XX WPI; 1999-120514/10.

PT Inducing a cytotoxic T lymphocyte response - by maintaining a level
 of antigen in the lymphatic system of a mammal so as to provide a
 sustained CTL response, used to treat, e.g. AIDS

XX Disclosure; Page 45; 199pp; English.

XX The present invention describes a method of inducing and/or sustaining
 CC an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The
 CC method comprises: (a) delivering an antigen to the mammal at a level to
 CC induce an immunological CTL response in the mammal; and (b) maintaining
 CC the level of the antigen in the mammal's lymphatic system to maintain
 CC the immunologic CTL response. The method can be used for the delivery of
 CC e.g. a differentiation antigen, a tumour-specific multineage antigen,
 CC an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor

CC gene antigen, or a viral antigen. They can be used for the treatment of
 CC disease such as cancer, e.g. malignant melanoma or infectious disease,
 CC e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery
 CC to the lymphatic system provides for potent CTL stimulation that takes
 CC place in the milieu of the lymphoid organ, and it sustains stimulation
 CC that is necessary to keep CTL active, cytotoxic and recirculating
 CC through the body. AAY10071 to AAY10639 represent examples of peptide
 CC antigens given in the present invention.

XX SQ Sequence 9 AA;

Alignment Scores:
 Pred. No.: 2.94e+07 Length: 9
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.86% Indels: 0
 DB: 20 Gaps: 0

US-09-824-647-16 (1-2095) x AAY10533 (1-9)

QY 918 GCGCTGGGCTGCTGCC 935

Db 3 GlyLeuGlyLeuLeuPro 8

RESULT 26

AAG67189

ID AAG67189 standard; peptide; 9 AA.

XX AAG67189;

XX

DT 13-NOV-2001 (first entry)

DE

XX Cancer testis tumour antigen NY-ESO-1 derived peptide.

XX Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
 KW HLA; HLA binding peptide; major histocompatibility complex; MHC;
 KW tumour; cancer; testis tumour.

XX Homo sapiens.

XX WO200162917-A1.

XX 30-AUG-2001.

XX 22-JAN-2001; 2001WO-US02126.

XX 22-FEB-2000; 2000US-0510635.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Lethe B, Boon-Falleur T;

XX WPI; 2001-550091/61.

XX Genomic sequences of tumour associated antigen NY-ESO-1 (LAGE-2) useful
 XX for diagnosing testicular tumours.

XX Example 13; Page 26; 50pp; English.

XX AAG67169-AAG67206 represent peptides which are derived from cancer
 CC testis tumour antigen NY-ESO-1 (also called LAGE-2). The peptides
 CC bind to human leukocyte antigens (HLAs). NY-ESO-1 is a molecule that
 CC is processed to at least one human leukocyte antigen (HLA) binding
 CC peptide, which binds to Class I and Class II major histocompatibility
 CC complex (MHC). NY-ESO-1 is expressed in tumour mRNA and in testis,
 CC but not normal colon, kidney, liver or brain tissue. The presence or
 CC level of expression of NY-ESO-1 may be assayed for the diagnosis of
 CC cancer, especially testis tumours.

XX SQ Sequence 9 AA;

Alignment Scores:

Pred. No.: 2.94e+07 Length: 9
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.86% Indels: 0
 DB: 22 Gaps: 0

US-09-824-647-16 (1-2095) x AAG67189 (1-9)

QY 1119 CAGCAGCTGCTCCTCCTC 1136

Db 1 GlyLeuLeuSerLeuLeu 6

RESULT 27

AAB85641

ID AAB85641 standard; peptide; 9 AA.

XX AAB85641;

XX

DT 29-OCT-2001 (first entry)

DE

XX Synthetic peptide immunoreactive with tau antibody HT7.

XX Tauopathy; phospho-tau (181); neurological marker; antibody; BT2; AT120;
 KW HT7; AT270; nootropic; neuroprotective; cerebroprotective; epitope.

XX Synthetic.

XX Homo sapiens.

XX WO200155725-A2.

XX 02-AUG-2001.

XX 18-JAN-2001; 2001WO-EP00560.

XX 24-JAN-2000; 2000EP-0870008.

XX 27-JAN-2000; 2000US-0178391.

XX 22-NOV-2000; 2000EP-0870280.

XX (INNO-) INNOGENETICS NV.

XX Vanmechelen E, Vanderstichele H;

XX WPI; 2001-476242/51.

XX Determining the ratio of phospho-tau / total tau is useful for
 XX diagnosing a tauopathy i.e. Alzheimer's disease or Pick's disease,
 XX versus a non tauopathy.

XX Example 1; Fig 1; 71pp; English.

XX The invention provides a method of diagnosis of tauopathies in an
 CC individual that comprises determining the ratio of phospho-tau (181)/
 CC total tau. Tau and phospho tau are useful as neurological markers for
 CC manufacture of a diagnostic kit for the diagnosis of a tauopathy and/or
 CC the differential diagnosis of a tauopathy versus a non tauopathy. A
 CC phospho-peptide liable to form an immunological complex with monoclonal
 CC antibody HT7 and MAB AT270 comprising at least the minimal epitope of HT7
 CC or AT270 is useful to measure phospho-tau levels and diagnose a tauopathy
 CC and/or for the differential diagnosis of a tauopathy versus a non
 CC tauopathy. The kit is useful for the diagnosis of Alzheimer's disease,
 CC Pick's disease, sporadic frontotemporal dementia and/or frontotemporal
 CC dementia with parkinsonism linked to chromosome 17, Creutzfeldt Jacob
 CC disease, stroke and/or neurotoxicity in patients with leukemia. The
 CC phosphopeptide kits and methods are useful for therapeutic monitoring and
 CC for determining the effectiveness of a treatment. Sequences AAB85641-64
 CC represent synthetic peptides immunoreactive to tau antibodies HT7, taul,
 CC BT2, AT120 and AT270.

XX SQ Sequence 9 AA;

Alignment Scores:

Pred. No.: 2.94e+07 Length: 9

Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.87% Indels: 0
 DB: 22 Gaps: 0

US-09-824-647-16 (1-2095) x AAB85641 (1-9)

QY 465 GGGGAGCAGCCCGCAGGA 448

DB 2 GlyAlaAlaProGly 7

RESULT 28

AAB85642

ID AAB85642 standard; peptide; 9 AA.

XX AC AAB85642;

XX DT 29-OCT-2001 (first entry)

XX DE Synthetic peptide immunoreactive with tau antibody HT7.

XX KW Taupathy; phospho-tau (181); neurological marker; antibody; BT2; AT120;
 KW HT7; AT270; nootropic; neuroprotective; cerobroprotective; epitope.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO200155725-A2.

XX PD 02-AUG-2001.

XX PF 18-JAN-2001; 2001WO-EP00560.

XX PR 24-JAN-2000; 2000EP-0870008.

XX PR 27-JAN-2000; 2000US-0178391.

XX PR 22-NOV-2000; 2000EP-0870280.

XX PA (INNO-) INNOGENETICS NV.

XX PI Vannechelen E, Vanderstichele H;

XX DR WPI; 2001-476242/51.

XX PT Determining the ratio of phospho-tau / total tau is useful for
 PT diagnosing a taupathy i.e. Alzheimer's disease or Pick's disease,
 PT versus a non taupathy -

XX PS Example 1; Fig 1; 71pp; English.

XX CC The invention provides a method of diagnosis of tauopathies in an
 CC individual that comprises determining the ratio of phospho-tau (181)/
 CC total tau. Tau and phospho tau are useful as neurological markers for the
 CC manufacture of a diagnostic kit for the diagnosis of a taupathy and/or
 CC the differential diagnosis of a taupathy versus a non taupathy. A
 CC phospho-peptide liable to form an immunological complex with monoclonal
 CC antibody HT7 and Mab AT270 comprising at least the minimal epitope of HT7
 CC or AT270 is useful to measure phospho-tau levels and diagnose a taupathy
 CC and/or for the differential diagnosis of a taupathy versus a non
 CC taupathy. The kit is useful for the diagnosis of Alzheimer's disease,
 CC Pick's disease, sporadic Frontotemporal dementia and/or Frontotemporal
 CC dementia with Parkinsonism linked to chromosome 17, Creutzfeldt Jacob
 CC disease, stroke and/or neurotoxicity in patients with leukemia. The
 CC phosphopeptide kits and methods are useful for therapeutic monitoring and
 CC for determining the effectiveness of a treatment. Sequences AAB85641-64
 CC BT2, AT120 and AT270.

XX SQ Sequence 9 AA;

Alignment Scores:

Pred. No.: 2.94e+07

Score: 6.00

Length: 9

Matches: 6

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.87% Indels: 0
 DB: 22 Gaps: 0

US-09-824-647-16 (1-2095) x AAB85642 (1-9)

QY 465 GGGGAGCAGCCCGCAGGA 448

DB 1 GlyAlaAlaProGly 6

RESULT 29

AAU02257

ID AAU02257 standard; Peptide; 9 AA.

XX AC AAU02257;

XX DT 29-AUG-2001 (first entry)

XX DE HLA binding TADG-16 peptide #33.

XX KW Human; extracellular serine protease; tumour antigen derived gene-16;
 KW TADG-16; ovarian carcinoma; breast cancer; lung cancer; colon cancer;
 KW prostate cancer; HLA type.

XX OS Homo sapiens.

XX PN WO200127257-A1.

XX PD 19-APR-2001.

XX PF 13-OCT-2000; 2000WO-US28558.

XX PR 14-OCT-1999; 99US-0418527.

XX PA (UTAR-) UNIV ARKANSAS.

XX PI O'Brien TJ, Underwood LJ, Shigemasa K;

XX DR WPI; 2001-273769/28.

XX PT New tumour antigen-derived gene-16 protein, useful for diagnosis and
 PT treatment of ovarian, breast, lung, colon and prostate cancer -

XX PS Example 8; Page 53; 124pp; English.

XX CC AAU02255-AAU02394 represent TADG-16 peptides which are tested for
 CC their binding affinity to the 8 haplotypes HLA A0201, HLA A0205,
 CC HLA A1, HLA A24, HLA B7, HLA B8, HLA B2702, and HLA B4403. Tumour
 CC antigen derived gene-16 protein, TADG-16 (AAU02253), is a novel human
 CC extracellular serine protease. TADG-16 is expressed in normal ovaries
 CC and testes and in certain ovarian carcinomas. TADG-16 contains the
 CC conserved catalytic triad, His-Asp-Ser, and a signal secretion sequence
 CC characteristic of the serine protease family. An antisense
 CC oligonucleotide having a complementary sequence to the TADG-16 nucleic
 CC acid is useful for treating various cancers, including ovarian, breast,
 CC lung, colon and prostate. The TADG-16 nucleic acid, TADG-16 protein and
 CC antibodies specific to TADG-16 are useful for the diagnosis of cancer.
 CC TADG-16 protein or its fragments are useful for vaccinating an individual
 CC against TADG-16.

XX SQ Sequence 9 AA;

Alignment Scores:

Pred. No.: 2.94e+07

Score: 6.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 0.87%

DB: 22

Length: 9

Matches: 6

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-09-824-647-16 (1-2095) x AAU02257 (1-9)

QY 884 GGCAGCTCACCTCCATG 867
 Db |||||||
 4 GlyGlnLeuThrSerMet 9

RESULT 30
 AAU02355
 ID AAU02355 standard; Peptide; 9 AA.
 XX
 AC AAU02355;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE HLA binding TADG-16 peptide #131.
 XX
 KW Human; extracellular serine protease; tumour antigen derived gene-16;
 KW TADG-16; ovarian carcinoma; breast cancer; lung cancer; colon cancer;
 KW prostate cancer; HLA type.
 XX
 OS Homo sapiens.
 XX
 PN WO200127257-A1.
 XX
 PD 19-APR-2001.
 XX
 PF 13-OCT-2000; 2000WO-US28558.
 XX
 PR 14-OCT-1999; 99US-0418527.
 XX
 PA (UYAR-) UNIV ARKANSAS.
 XX
 PI O'Brien TJ, Underwood LJ, Shigemasa K;
 XX WPI; 2001-273769/28.
 DR
 XX New tumour antigen-derived gene-16 protein, useful for diagnosis and
 XX treatment of ovarian, breast, lung, colon and prostate cancer -
 XX
 PS Example 8; Page 55; 124pp; English.
 XX
 CC AAU02225-AAU02384 represent TADG-16 peptides which are tested for
 CC their binding affinity to the 8 haplotypes HLA A0201, HLA A0205,
 CC HLA A1, HLA A24, HLA B7, HLA B8, HLA B2702, and HLA B4403. Tumour
 CC antigen derived gene-16 protein, TADG-16 (AAU02223), is a novel human
 CC extracellular serine protease. TADG-16 is expressed in normal ovaries
 CC and testes and in certain ovarian carcinomas. TADG-16 contains the
 CC conserved catalytic triad, His-Asp-Ser, and a signal secretion sequence
 CC characteristic of the serine protease family. An antisense
 CC oligonucleotide having a complementary sequence to the TADG-16 nucleic
 CC acid is useful for treating various cancers, including ovarian, breast,
 CC lung, colon and prostate. The TADG-16 nucleic acid, TADG-16 protein and
 CC antibodies specific to TADG-16 are useful for the diagnosis of cancer.
 CC TADG-16 protein or its fragments are useful for vaccinating an individual
 CC against TADG-16.
 XX
 SQ Sequence 9 AA;
 Alignment Scores:
 Pred. No.: 2.94e+07 Length: 9
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.87% Indels: 0
 DB: 22 Gaps: 0

US-09-824-647-16 (1-2095) x AAU02355 (1-9)

QY 884 GGCAGCTCACCTCCATG 867
 Db |||||||
 1 GlyGlnLeuThrSerMet 6

RESULT 31
 AAU02360
 ID AAU02360 standard; Peptide; 9 AA.

XX
 AC
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE HLA binding TADG-16 peptide #136.
 XX
 KW Human; extracellular serine protease; tumour antigen derived gene-16;
 KW TADG-16; ovarian carcinoma; breast cancer; lung cancer; colon cancer;
 KW prostate cancer; HLA type.
 XX
 OS Homo sapiens.
 XX
 PN WO200127257-A1.
 XX
 PD 19-APR-2001.
 XX
 PF 13-OCT-2000; 2000WO-US28558.
 XX
 PR 14-OCT-1999; 99US-0418527.
 XX
 PA (UYAR-) UNIV ARKANSAS.
 XX
 PI O'Brien TJ, Underwood LJ, Shigemasa K;
 XX WPI; 2001-273769/28.
 DR
 XX New tumour antigen-derived gene-16 protein, useful for diagnosis and
 XX treatment of ovarian, breast, lung, colon and prostate cancer -
 XX
 PS Example 8; Page 55; 124pp; English.
 XX
 CC AAU02225-AAU02384 represent TADG-16 peptides which are tested for
 CC their binding affinity to the 8 haplotypes HLA A0201, HLA A0205,
 CC HLA A1, HLA A24, HLA B7, HLA B8, HLA B2702, and HLA B4403. Tumour
 CC antigen derived gene-16 protein, TADG-16 (AAU02223), is a novel human
 CC extracellular serine protease. TADG-16 is expressed in normal ovaries
 CC and testes and in certain ovarian carcinomas. TADG-16 contains the
 CC conserved catalytic triad, His-Asp-Ser, and a signal secretion sequence
 CC characteristic of the serine protease family. An antisense
 CC oligonucleotide having a complementary sequence to the TADG-16 nucleic
 CC acid is useful for treating various cancers, including ovarian, breast,
 CC lung, colon and prostate. The TADG-16 nucleic acid, TADG-16 protein and
 CC antibodies specific to TADG-16 are useful for the diagnosis of cancer.
 CC TADG-16 protein or its fragments are useful for vaccinating an individual
 CC against TADG-16.
 XX
 SQ Sequence 9 AA;
 Alignment Scores:
 Pred. No.: 2.94e+07 Length: 9
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.87% Indels: 0
 DB: 22 Gaps: 0

US-09-824-647-16 (1-2095) x AAU02360 (1-9)

QY 884 GGCAGCTCACCTCCATG 867
 Db |||||||
 4 GlyGlnLeuThrSerMet 9

RESULT 32
 AAB69921
 ID AAB69921 standard; Peptide; 9 AA.
 XX
 AC AAB69921;
 XX
 DT 27-APR-2001 (first entry)
 XX
 DE Human NY-ESO-1 HLA binding motif #21.
 XX

us-09-824-647-16.lim.rag

Tue Jul 8 07:45:06 2003

KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
 KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
 KW non-small cell lung carcinoma; tumour status determination.
 XX Homo sapiens.
 OS
 XX WO200107917-A1.
 PN
 XX
 XX 01-FEB-2001.
 PD
 XX
 XX 14-JUL-2000; 2000WO-US19220.
 PF
 XX
 XX 23-JUL-1999; 99US-0359503.
 PR
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 PA (CORR) CORNELL RES FOUND INC.
 XX
 XX Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
 PI
 XX
 XX WPI; 2001-182822/18.
 DR
 XX
 XX Method useful for determining the status (e.g. progression, regression
 PT or stability of the disease) of a cancerous condition, involves
 PT determining the levels of NY-ESO-1 specific antibodies in a sample
 PT taken from a patient
 XX
 XX Example 14; Page 25; 50pp; English.
 FS
 XX
 XX The present sequence is given in a specification relating to a method
 CC for determining the status of a cancerous condition in a patient
 CC with a tumour that expresses NY-ESO-1. The method comprises assaying a
 CC sample taken from the patient for antibodies that specifically bind to
 CC the NY-ESO-1 and comparing the value obtained to a prior value obtained
 CC from assay of a prior sample taken from the patient. Any difference
 CC between the values is indicative of a change in status of the cancerous
 CC condition. The method is useful for determining whether a cancerous
 CC condition is progressing, regressing or remaining stable, in particular
 CC in patients receiving treatment for a melanoma, adenocarcinoma,
 CC non-small cell lung carcinoma or bladder carcinoma.
 XX
 XX Sequence 9 AA;
 SQ
 Alignment Scores:
 Pred. No.: 2.94e+07 Length: 9
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.86% Indels: 0
 DB: 22 Gaps: 0
 US-09-824-647-16 (1-2095) x AAB69921 (1-9)
 QY 1119 CAGCAGCTCTCTCTCTC 1136
 DB 1 GlnGlnLeuSerLeuLeu. 6
 RESULT 33
 AAU95803
 ID AAU95803 standard; Peptide; 9 AA.
 XX
 XX AAU95803;
 AC
 XX
 XX 02-JUL-2002 (first entry)
 DT
 XX
 XX Immunogenic peptide with (HLA)-A2.1 binding site #16.
 DE
 XX HLA-A2.1 binding peptide; cytostatic; virucide; anti-HIV; hepatotropic;
 KW human immunodeficiency virus; antiinflammatory; antibacterial; vaccine;
 KW protozoacide; immunosuppressant; immunogenic peptide; T cell activation;
 KW human leukocyte antigen binding site; cytotoxic T cell response;
 KW viral infection; hepatitis; Epstein-Barr virus; papilloma virus;
 KW human immunodeficiency virus; HIV; Kaposi sarcoma; Lassa fever virus;

KW cytomegalovirus; tumour; prostate cancer; renal carcinoma; lymphoma;
 KW prostate-specific antigen; p53; carcino-embryonal antigen;
 KW melanoma antigen; Mycobacterium tuberculosis; protozoa;
 KW trypanosome surface antigen; condyloma acuminatum.
 XX
 XX Mycobacterium tuberculosis.
 OS
 XX WO200220616-A1.
 PN
 XX
 XX 14-MAR-2002.
 PD
 XX
 XX 01-SEP-2000; 2000WO-US24102.
 PF
 XX
 XX 01-SEP-2000; 2000WO-US24102.
 PR
 XX
 XX (EPIM-) EPIMUNE INC.
 PA
 XX
 XX Grey HM, Sette A, Sidney J, Southwood S;
 PI
 XX
 XX WPI; 2002-351746/38.
 DR
 XX
 XX Immunogenic peptide with human leucocyte antigen-A2.1 binding site,
 PT useful for treating e.g. viral infection or tumours
 PT
 XX
 XX Claim 1; Page 24; 35pp; English.
 PS
 XX
 XX The invention describes a composition comprising an immunogenic peptide
 CC having a human leucocyte antigen (HLA)-A2.1 binding site. The peptides
 CC bind specifically to HLA-A2.1, to cause T cell activation and thus a
 CC cytotoxic T cell response. The peptides and the nucleic acids that
 CC encode them, are used, in vivo or ex vivo, for treatment of viral
 CC infections (hepatitis B or C; Epstein-Barr; human immune deficiency;
 CC Kaposi sarcoma; human papilloma; Lassa fever or cytomegalovirus);
 CC tumours including prostate cancer, renal carcinoma and lymphoma (where
 CC directed to prostate-specific antigen, p53, carcino-embryonal antigen,
 CC Her2/neu or melanoma antigens); infection by Mycobacterium tuberculosis
 CC or protozoa (directed to trypanosome surface antigen); and condyloma
 CC acuminatum. The peptides are suitable for use in peptide-based
 CC vaccines. This sequence represents an immunogenic peptide with the
 CC human leucocyte antigen (HLA)-A2.1 binding site, described in the
 CC invention.
 XX
 XX Sequence 9 AA;
 SQ
 Alignment Scores:
 Pred. No.: 2.94e+07 Length: 9
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.87% Indels: 0
 DB: 23 Gaps: 0
 US-09-824-647-16 (1-2095) x AAU95803 (1-9)
 QY 144 GGCAGCGCAGCAGCTGTA 127
 DB 4 GlyThrAlaAlaAlaVal 9
 RESULT 34
 AAU90829
 ID AAP90829 standard; protein; 10 AA.
 XX
 XX AAP90829;
 AC
 XX
 XX 29-JUN-1990 (first entry)
 DT
 XX
 XX New bradykinin analogue with D-beta-(2-naphthyl)-Ala,
 DE beta-(2-thienyl)-Ala and D-Phe.
 DE
 XX
 XX Bradykinin analogue; bradykinin antagonist.
 KW
 XX
 XX Key Location/Qualifiers
 FH
 FT Misc-difference 1

FT /label-OTHER
 FT /note="D-beta-(2-naphthyl)-Ala"
 FT Misc-difference 2
 FT /label-OTHER
 FT /note="As above"
 FT Misc-difference 6
 FT /label-OTHER
 FT /note="beta-(2-thienyl)-Ala"
 FT Misc-difference 9
 FT /label-OTHER
 FT /note="As above"
 FT Misc-difference 8
 FT /label-D-Phe

PN W08901781-A.

XX 09-MAR-1989.

XX 29-AUG-1988; 88WO-US02960.

XX 02-SEP-1987; 87US-0091995.

XX (STEW/) STEWART JM.

XX Stewart JM, Vavrek RJ;

XX WPI; 1989-085401/11.

XX New peptide bradykinin analogues -
 PT with D-amino acid in 7 position, useful as bradykinin antagonists
 XX Claim 10; page 52; 54pp; English.

XX It may be prep'd. by conventional liq. - or solid-phase peptide
 CC synthesis methods. It is useful for treating local pain, inflammation
 CC and swelling, rhinitis, hypotension, asthma, arthritis, diarrhoea,
 CC irritable bowel syndrome, carcinoid syndrome, angina pain, and
 CC anaphylactic or septic shock. Pharmaceutical compns. can be made with
 CC it.

XX Sequence 10 AA;

Alignment Scores:
 Pred. No.: 1.88e+04 Length: 10
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.87% Indels: 0
 DB: 10 Gaps: 0

US-09-824-647-16 (1-2095) x AAP90829 (1-10)

QY 462 GCAGCACCAGGAGCC 445

Db 1 AlaAlaProGlyAla 6

RESULT 35

AAR93340

ID AAR93340 standard; peptide; 10 AA.

XX AAR93340;

XX 24-APR-1996 (first entry)

XX TSK protein tyrosine kinase derived peptide #4.

XX SH3 ligand; SH3 binding agent; biased phage library;
 KW recognition sequence; src SH3 domain; Paget's disease; restenosis;
 KW rheumatoid arthritis; gout; neutrophil oxidase; tyrosine kinase; p47;
 KW p67; complex; chronic myelogenous leukaemia; cancer.
 XX Synthetic.

XX

PN W09524419-A1.

XX 14-SEP-1995.

XX 13-MAR-1995; 95WO-US03208.

XX 06-JAN-1995; 95US-0369832.

XX 11-MAR-1994; 94US-0209835.

XX (ARIA-) ARIAD PHARM INC.

XX Botfield MC; Brugge JS, Rickles RJ, Zoller MJ;

XX WPI; 1995-328231/42.

XX Identification of peptide(s) binding specifically to SH3 domains -
 PT for use in inhibiting interactions mediated by SH3 domains in
 PT treatment of e.g. osteoporosis and cancer

XX Disclosure; Fig 1; 74pp; English.

XX The sequences given in AAR93272-342 represent peptides which are SH3
 CC ligands/SH3 binding agents. They represent a biased phage library
 CC which comprises six random amino acids flanking the tetrapeptide
 CC -PPIP which was identified as a recognition sequence for the src SH3
 CC domain. These sequences were identified using the method of the
 CC invention. The method comprises contacting the SH3 domain with a
 CC mixture of peptides under conditions permitting a ligand to bind to
 CC an SH3 domain to form a complex. Any unbound peptides are removed
 CC and the complexed peptide ligands are dissociated from the complexes.
 CC The selected peptides are enriched by re-contacting them with the
 CC SH3 domain and then candidates which bind to the SH3 domain are
 CC detected. The isolated SH3 binding peptides may be used in the
 CC diagnosis, prevention and treatment of conditions or diseases resulting
 CC from cellular processes mediated by an SH3-based interaction. Such
 CC diseases include Paget's disease. Other conditions treatable with these
 CC peptides include restenosis, rheumatoid arthritis, gout and other
 CC problems in which an SH3 of neutrophil oxidase p47 and p67 complex is
 CC implicated, etc.

XX Sequence 10 AA;

Alignment Scores:
 Pred. No.: 1.88e+04 Length: 10
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.86% Indels: 0
 DB: 16 Gaps: 0

US-09-824-647-16 (1-2095) x AAR93340 (1-10)

QY 1127 GTCCCTCTCCGATACCT 1144

Db 5 ValProProGlyPro 10

RESULT 36

AAR66370

ID AAR66370 standard; peptide; 10 AA.

XX AAR66370;

XX 27-JUN-1995 (first entry)

XX Chlamydial MOMP VDI epitope.

XX Chlamydial epitope; variable domain; MOMP;

XX major outer membrane protein; picornavirus; poliovirus; pV1;

XX diagnostic; therapeutic; capsid protein.

XX Chlamydia trachomatis serovar A.

XX W09426900-A.

XX PD 24-NOV-1994.
XX PF 12-MAY-1994; 94WO-CR00262.
XX PR 13-MAY-1993; 93US-0060978.
XX PA (CONN-) CONNAUGHT LAB LTD.
XX PI Caldwell HD, Klein MH, Murdin AD, Oomen RP;
XX WPI; 1995-006796/01.
XX New hybrid picornaviruses expressing chlamydial epitopes - used
PT to develop prods. for vaccination, diagnosis, treatment of
PT chlamydial infections and prodn. of immunological reagents
XX Disclosure; Page 15; 99pp; English.
XX To obtain a poliovirus-1 (PV1)/chlamydial hybrid, the PV1
CC Mahoney cDNA clone pF7XLD was modified to encode epitopes from
CC C. trachomatis ser. A MOMP VDI. The mutagenesis cartridge was
CC contained between PV nucleotides 2753-91 (given in AAQ79003) which
CC encode PV amino acids 1092-1104 (AAR66375) which include the BC loop
CC of capsid protein VP1 (AAR66386). The polio-specific DNA within the
CC cartridge, encoding the sequence given in AAR66369, was replaced by
CC oligonucleotides encoding VDI peptides AAR66370-74. Viable PV
CC expressing chlamydial immunostimulatory epitope was expressed in
CC Vero cells.
XX SQ Sequence 10 AA;
Alignment Scores:
Pred. No.: 1.88e+04 Length: 10
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 16 Gaps: 0
US-09-824-647-16 (1-2095) x AAR66370 (1-10)
OY 1279 GTGGCTGGACTGGAGAG 1296
DB 1 ValAlaGlyLeuGluLys 6
RESULT 37
AAW42311
ID AAW42311 standard; Peptide; 10 AA.
XX AC AAW42311;
XX DT 08-APR-1998 (first entry)
XX DE D-form Interleukin-8 peptide ligand consensus sequence 2.
XX KW Bacteriophage peptide library; peptide epitope; therapeutic target;
XX KW variegated compound library; interleukin-8; IL-8.
XX OS Synthetic.
XX PN WO9735194-A2.
XX PD 25-SEP-1997.
XX PF 21-MAR-1997; 97WO-US04176.
XX PR 21-MAR-1996; 96US-0622338.
XX PA (HARD) HARVARD COLLEGE.
XX PI Forster AC;
XX PA

DR WPI; 1997-480355/44.
XX Identifying compounds which interact with target molecules - using
PT enantiomers of the target molecules and testing of enantiomers of
PT selected compounds.
XX Disclosure; Fig 8; 89pp; English.
XX The present sequence represents a consensus sequence obtained after
CC several rounds of selection and amplification of a 6-mer peptide library.
CC The consensus sequence is derived from peptide ligands of a D-enantiomer
CC of interleukin-8 (IL-8), and was obtained using the method of the
CC invention. This novel method identifies compounds which interact with a
CC target molecule, and comprises contacting a screening molecule with a
CC variegated compound library, where the screening molecule comprises solid
CC target molecule, or the enantiomer if the target molecule is chiral.
CC Compounds which have a desired interaction with the target molecule are
CC selected, and the ability of their enantiomer to interact with the target
CC molecule is tested. Ligands for a target protein (a D-target protein), and a
CC combining a D-enantiomer of a target protein (a D-target protein), and a
CC variegated compound library, and then selecting one or more compounds
CC from the library which have a desired binding interaction with the
CC D-target protein. The methods can be used for identifying agonists or
CC antagonists of targets such as receptors, enzymes, DNA binding proteins
CC or signal transduction proteins. The methods can provide a structurally
CC selective approach in addition to scoring for interaction of functional
CC groups. They provide a powerful selection method that allows for the
CC production of ligands with the same diversity as peptides but with the
CC greatly improved pharmacokinetic profiles needed for drug activity.
XX SQ Sequence 10 AA;
Alignment Scores:
Pred. No.: 1.88e+04 Length: 10
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.87% Indels: 0
DB: 18 Gaps: 0
US-09-824-647-16 (1-2095) x AAW42311 (1-10)
OY 741 GTGATCGGAGCAGCAGGT 724
DB 5 ValIleGlyAlaAlaGly 10
RESULT 38
AAW82826
ID AAW82826 standard; peptide; 10 AA.
XX AC AAW82826;
XX DT 28-JAN-1999 (first entry)
XX DE Cytomodulating lipophilic oligopeptide (w).
XX KW Cytomodulating lipophilic oligopeptide; Immune system; inflammation;
XX KW cytotoxic; lymphocytic; inhibition; cytokine; autoimmune disease; T cell;
XX KW B cell; mononuclear phagocyte; septic shock; rheumatoid arthritis;
XX KW Crohn's disease; colitis; allergy; transplant.
XX OS Synthetic.
XX PN WO9846633-A1.
XX PD 22-OCT-1998.
XX PF 10-APR-1998; 98WO-US07231.
XX PR 23-FEB-1998; 98US-0028083.
XX PR 11-APR-1997; 97US-0838916.
XX PA (SANG-) SANGSTAT MEDICAL CORP.

XX Buelow R, Calas B, Grassy G;
 XX WPI; 1998-594558/50.
 XX New lipophilic peptide(s) that inhibit activation of immune system
 PT cells - used for, e.g. production of cytokine(s) and the
 PT inflammatory response, and also for modulating haem-containing
 PT enzymes
 XX
 XX Claim 7; Page 37; 48pp; English.
 XX
 XX AAW82804 to AAW82829 are cytomodulating lipophilic oligopeptides. The
 CC oligopeptides are used to inhibit: (i) activity of lymphocytes
 CC (particularly cytotoxic T cells, but also natural killers, B cells and
 CC mononuclear phagocytes); (ii) production of inflammatory cytokines, and
 CC (iii) an inflammatory response in mammals (e.g. in cases of septic
 CC shock, rheumatoid arthritis (RA), Crohn's disease, colitis and allergy).
 CC They are also used for modulating activity of haem-containing enzymes and
 CC for delaying onset of autoimmune disease (specifically insulin-dependent
 CC diabetes mellitus, RA and systemic lupus erythematosus). In all cases
 CC the oligopeptides may be generated from nucleic acids, and treatments
 CC are in vitro or in vivo. A specific application is treatment of organs
 CC or cells for transplantation, or of the recipient of such transplants.
 CC Apart from therapeutic use, the oligopeptides can be used to study
 CC mechanisms of T cell (de)activation and to raise antibodies (used to
 CC identify oligopeptides and to raise anti-idiotypic antibodies that are
 CC competitors of the oligopeptides. The oligopeptides are administered by
 CC bolus injection or infusion, typically at 0.1-50 (preferably 1-25)
 CC mg/kg. Treatment with the oligopeptides increases the life of
 CC transplants.
 XX

SO Sequence 10 AA;

Alignment Scores:
 Pred. No.: 1.88e+04 Length: 10
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.86% Indels: 0
 DB: 19 Gaps: 0

US-09-824-647-16 (1-2095) x AAW82826 (1-10)

QY 1131 CTCTCCGATACCTGCTG 1148

DB 3 LeuLeuArgTyrLeuLeu 8

RESULT 39

AY05999
 ID AAY05999 standard; Peptide; 10 AA.

AC AAY05999;

DT 16-AUG-1999 (first entry)

DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine; human leukocyte antigen; HLA.

XX Homo sapiens.

OS WO9918206-A2.

PN 15-APR-1999.

PD 21-SEP-1998;

XX 98WO-US19609.

XX 08-OCT-1997; 97US-0061428.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX

PI Rosenberg SA, Wang RF;

XX WPI; 1999-277270/23.

XX Cancer antigen NY ESO1/CAG-3

XX Example 10; Page 42; 88pp; English.

XX This peptide was identified as an HLA peptide motif following a
 CC screen for epitopes from the coding region of human ESO-1/CAG-3
 CC ORF1 (see AAY58599). 30 Epitopes (see AAY05988-Y06017) were identified.
 CC The present peptide (ranked 12) corresponds to amino acid residues
 CC 152-161 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
 CC tumour antigen capable of eliciting an antigen specific immune
 CC response by T cells. Cancer peptides (see AAY05967-87) derived from
 CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
 CC vaccines. A claimed method of preventing or inhibiting cancer
 CC involves administering a cancer peptide, with or without an HLA
 CC molecule. The cancer peptides form part of, or are derived
 CC from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
 CC cancer, cervical cancer, bladder cancer, kidney cancer and
 CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
 CC thyroid cancers.

XX Sequence 10 AA;

Alignment Scores:
 Pred. No.: 1.88e+04 Length: 10
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.86% Indels: 0
 DB: 20 Gaps: 0

US-09-824-647-16 (1-2095) x AAY05999 (1-10)

QY 1119 CAGCAGCTGCTCCCTCTC 1136

DB 3 GlnGlnLeuSerLeuLeu 8

RESULT 40

AY06009
 ID AAY06009 standard; Peptide; 10 AA.

AC AAY06009;

DT 16-AUG-1999 (first entry)

DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine; human leukocyte antigen; HLA.

XX Homo sapiens.

OS WO9918206-A2.

PN 15-APR-1999.

PD 21-SEP-1998;

XX 98WO-US19609.

XX 08-OCT-1997; 97US-0061428.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Rosenberg SA, Wang RF;

XX DR WPI; 1999-277270/23.

XX PT Cancer antigen NY ESO1/CAG-3

XX PS Example 10; Page 42; 89pp; English.

XX CC This peptide was identified as an HLA peptide motif following a
XX CC screen for epitopes from the coding region of human ESO-1/CAG-3
XX CC ORF1 (see AAY58599). 30 Epitopes (see AAY05988-Y06017) were identified.
XX CC The present peptide (ranked 22) corresponds to amino acid residues
XX CC 154-163 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
XX CC tumour antigen capable of eliciting an antigen specific immune
XX CC response by T cells. Cancer peptides (see AAY05967-87) derived from
XX CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
XX CC vaccines. A claimed method of preventing or inhibiting cancer
XX CC involves administering a cancer peptide, with or without an HLA
XX CC molecule. The cancer peptides form part of, or are derived
XX CC from, cancers such as primary or metastatic melanoma, thymoma,
XX CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
XX CC cancer, cervical cancer, bladder cancer, kidney cancer and
XX CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
XX CC thyroid cancers.

XX SQ Sequence 10 AA;

Alignment Scores: Length: 10
Pred. No.: 1.88e+04
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 20 Gaps: 0

US-09-824-647-16 (1-2095) x AAY06009 (1-10)

OY 1119 CAGCAGCTGCTCCTCTC 1136

DB 1 GlnGlnLeuSerLeuLeu 6

RESULT 41

AAY05997

ID AAY05997 standard; Peptide; 10 AA.

XX AC AAY05997;

XX DT 16-AUG-1999 (first entry)

XX DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.

XX KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
XX KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
XX KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
XX KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
XX KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
XX KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
XX KW vaccine; human leukocyte antigen; HLA.

XX OS Homo sapiens.

XX PN WO9918206-A2.

XX PD 15-APR-1999.

XX PF 21-SEP-1998; 98WO-0519609.

XX PR 08-OCT-1997; 97US-0061428.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Rosenberg SA, Wang RF;

XX DR WPI; 1999-277270/23.

XX PT Cancer antigen NY ESO1/CAG-3

XX PS Example 10; Page 42; 88pp; English.

XX CC This peptide was identified as an HLA peptide motif following a
XX CC screen for epitopes from the coding region of human ESO-1/CAG-3
XX CC ORF1 (see AAY58599). 30 Epitopes (see AAY05988-Y06017) were identified.
XX CC The present peptide (ranked 10) corresponds to amino acid residues
XX CC 153-162 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
XX CC tumour antigen capable of eliciting an antigen specific immune
XX CC response by T cells. Cancer peptides (see AAY05967-87) derived from
XX CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
XX CC vaccines. A claimed method of preventing or inhibiting cancer
XX CC involves administering a cancer peptide, with or without an HLA
XX CC molecule. The cancer peptides form part of, or are derived
XX CC from, cancers such as primary or metastatic melanoma, thymoma,
XX CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
XX CC cancer, cervical cancer, bladder cancer, kidney cancer and
XX CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
XX CC thyroid cancers.

XX SQ Sequence 10 AA;

Alignment Scores: Length: 10
Pred. No.: 1.88e+04
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 20 Gaps: 0

US-09-824-647-16 (1-2095) x AAY05997 (1-10)

OY 1119 CAGCAGCTGCTCCTCTC 1136

DB 2 GlnGlnLeuSerLeuLeu 7

RESULT 42

AAY13579

ID AAY13579 standard; peptide; 10 AA.

XX AC AAY13579;

XX DT 30-JUL-1999 (first entry)

XX DE Peptide sensor TUK-1473.

XX KW Nuclear hormone receptor; sensor peptide; receptor binding; screening;
XX KW modulator.

XX OS Synthetic.

XX PN WO9927365-A1.

XX PD 03-JUN-1999.

XX PF 20-NOV-1998; 98WO-US24969.

XX PR 30-SEP-1998; 98US-0163713.

XX PR 21-NOV-1997; 97US-0975614.

XX PA (TULA-) TULARIK INC.

XX PI Baerle P, Beckmann H, Chen J, Lustig K, Shan B;

XX DR WPI; 1999-347794/29.

XX PT Nuclear hormone receptor drug screens

XX Claim 7; Page 18; 29pp; English.
 XX The invention provides methods for screening of modulators of nuclear
 CC hormone receptor function. The methods use a sensor peptide covalently
 CC coupled to a detectable label, that provides direct, in vitro ligand-
 CC dependent binding to a nuclear hormone receptor. Panels of predetermined
 CC or randomized candidate sensors are readily screened for receptor
 CC binding. The methods and compositions provide for efficient screening of
 CC modulators of nuclear hormone receptor function, without the use of
 CC cell- or gel-based steps. The methods are amenable to automated,
 CC cost-effective high throughput screening of chemical libraries for
 CC bioactive compounds. To ensure specificity and optimize binding, the
 CC sensor is generally present at sub-micromolar concentration and the
 CC binding reaction occurs in solution. The sensor peptide obviates the need
 CC to include a natural coactivator protein of the receptor in the mixture.
 CC Sequences AAY13571-587 represent examples of sensor peptides that can be
 CC used in the method of the invention.

XX Sequence 10 AA;

Alignment Scores:
 Pred. No.: 1.88e+04 Length: 10
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.86% Indels: 0
 DB: 20 Gaps: 0

US-09-824-647-16 (1-2095) x AAY13579 (1-10)

QY 1131 CTCCTCCGATACCTGCTG 1148

DB 2: LeuLeuArgTyrLeuLeu 7

RESULT 43

AAW93872

ID AAW93872 standard; peptide; 10 AA.

AC AAW93872;

DT 25-JUN-1999 (first entry)

DE Bifidobacterium bifidus stimulating peptide 8.

XX Bifidogenic peptide; protease; treatment; microbe-related disease;
 KW bacteria; fungi; yeast; protozoa; virus; mycoplasma; filaria; plasmodia;
 KW infection; inflammation; microbial induced tumour; degenerative disorder;
 KW diarrhoea; colic; oral microflora; intestinal microflora; caries;
 KW vaginal microflora.

OS Bifidobacterium bifidus.

PN WO9914231-A2.

XX 25-MAR-1999.

PF 16-SEP-1998; 98WO-EP05899.

XX 11-FEB-1998; 98DE-1005385.

PR 16-SEP-1997; 97DE-1040604.

XX (FORS/) FORSMANN W.

XX Forssmann W, Liepke C, Zucht H;

DR WPI; 1999-244022/20.

PT Milk-derived peptides that stimulate Bifidobacterium bifidus

XX Claim 2; Page 3; 25pp; German.

CC This invention describes milk-derived bifidogenic peptides and their

CC active derivatives or fragments, and combinations of them produced by
 CC chemical coupling. Such are produced from bovine or human milk by
 CC treatment for 2 hr with proteases, then centrifuging to remove fat and
 CC acidifying to pH 2 to precipitate proteins. The solution phase is then
 CC subjected to reverse-phase high-performance liquid chromatography (HPLC)
 CC and cation-exchange HPLC, the fractions adjusted to salt content below
 CC 25 mM (by dialysis or reverse-phase HPLC) and tested for activity by
 CC growing Bifidobacterium bifidus and Escherichia coli in presence of the
 CC fractions. Those fractions for which (Bw-B0)-(Ew-E0) is at least 0.15
 CC are selected where Bw = germ count after 16 hr culture of B. bifidus in
 CC 50% Elliker broth containing peptide at 0.2 mg/ml, B0 = germ count under
 CC similar conditions in a peptide-free control, Ew = germ count after 16
 CC hr culture of E. coli in 3 g/l tryptic broth containing peptide at
 CC 0.2 mg/ml, E0 = germ count under similar conditions in a peptide-free
 CC control. The peptides AAW93865-W93888 are used to treat microbe-related
 CC diseases caused by bacteria, fungi, yeast, protozoa, viruses,
 CC mycoplasma, filaria and plasmodia, e.g. infections, inflammation,
 CC microbially induced tumours or degenerative disorders, diarrhoea, colic,
 CC abnormalities in oral, intestinal or vaginal microflora, or caries.

XX Sequence 10 AA;

Alignment Scores:
 Pred. No.: 1.88e+04 Length: 10
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.86% Indels: 0
 DB: 20 Gaps: 0

US-09-824-647-16 (1-2095) x AAW93872 (1-10)

QY 1379 GTCGCCGAGCCAGGCTG 1396

DB 3 AlaAlaArgAlaArgVal 8

RESULT 44

AAW74014

ID AAW74014 standard; peptide; 10 AA.

AC AAW74014;

DT 04-MAY-1999 (first entry)

DE C. trachomatis MOMP epitope A-20.

XX Variable domain; MOMP; major outer membrane protein; subunit vaccine;

KW C. trachomatis infection; serotyping; diagnosis.

XX Chlamydia trachomatis.

OS US5869608-A.

PN 09-FEB-1999.

PF 16-MAR-1992; 92US-0853359.

XX 17-MAR-1989; 89US-0324664.

PR 16-MAR-1992; 92US-0853359.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Caldwell HD, Watkins NG, Ying Y, Zhang Y;

XX WPI; 1999-152876/13.

XX Chlamydia trachomatis peptides - and DNA fragments encoding them

PT Disclosure; Column 11-12; 29pp; English.

XX This sequence represents an epitope of the major outer membrane

CC protein (MOMP) of Chlamydia trachomatis. The invention relates

CC to variable domain fragments of the MOMP of Chlamydia trachomatis

CC serovar Ba, serovar D, serovar E, serovar F, serovar G, serovar H,
 CC serovar I, serovar J, serovar K, and serovar L3, and to DNA sequences
 CC encoding them. The peptides are useful in diagnostic tests for
 CC C. trachomatis infections, serological tests for serotyping, and as
 CC subunit vaccines.

XX
 SQ Sequence 10 AA;

Alignment Scores:
 Pred. No.: 1.88e+04 Length: 10
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.86% Indels: 0
 DB: 20 Gaps: 0

US-09-824-647-16 (1-2095) x AAW74014 (1-10)

QY 1279 GTGCTGGAGTGGAGAG 1296

DB 2 ValAlaGlyLeuGluLys 7

RESULT 45

AAG67204

ID AAG67204 standard; peptide; 10 AA.

XX AC AAG67204;

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Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.86% Indels: 0
 DB: 22 Gaps: 0

US-09-824-647-16 (1-2095) x AAG67204 (1-10)

QY 1119 CAGCAGCTGCTCCCTCCTC 1136

DB 1 GluGlnLeuSerLeuLeu 6

Search completed: July 7, 2003, 16:07:23
 Job time : 94 secs

Genomic sequences of tumour associated antigen EY-ESO-1 (LAGE-2) useful
 for diagnosing testicular tumours -

Example 13; Page 26; 50pp; English.

AAG67169-AAG67206 represent peptides which are derived from cancer
 testis tumour antigen NY-ESO-1 (also called LAGE-2). The peptides
 bind to human leukocyte antigens (HLAs). NY-ESO-1 is a molecule that
 is processed to at least one human leukocyte antigen (HLA) binding
 peptide, which binds to Class I and Class II major histocompatibility
 complex (MHC). NY-ESO-1 is expressed in tumour mRNA and in testis,
 but not normal colon, kidney, liver or brain tissue. The presence or
 level of expression of NY-ESO-1 may be assayed for the diagnosis of
 cancer, especially testis tumours.

XX Sequence 10 AA;

Alignment Scores:
 Pred. No.: 1.88e+04 Length: 10
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0

Pred. No.: 0.000925 Length: 14
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-824-647-7 (1-14)

QY 1708 GCACGAGGGTACCAAGTGTTCGCGAGGAGGCCCGCGC 1749
Db 1 AlaArgArgGlyThrLysCysLeuArgArgGluAlaProArg 14
|||||

RESULT 2

US-10-218-509-7.
; Sequence 7, Application US/10218509
; Publication No. US20030092661A1
; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: Z9996.488/P001-A
; CURRENT APPLICATION NUMBER: US/10/218,509
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 08/991,862
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Human granulin
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)-(14)
; OTHER INFORMATION: Internal peptide of human GP88 used to develop
; OTHER INFORMATION: Neutralizing anti-human GP88 monoclonal antibody.
US-10-218-509-7

Alignment Scores:
Pred. No.: 0.000925 Length: 14
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-10-218-509-7 (1-14)

QY 1708 GCACGAGGGTACCAAGTGTTCGCGAGGAGGCCCGCGC 1749
Db 1 AlaArgArgGlyThrLysCysLeuArgArgGluAlaProArg 14
|||||

RESULT 3

US-10-281-160-7
; Sequence 7, Application US/10281160
; Publication No. US20030108950A1
; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: Z9996.488/P001-A
; CURRENT APPLICATION NUMBER: US/10/281,160
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 08/991,862
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT

; ORGANISM: Human granulin
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)-(14)
; OTHER INFORMATION: Internal peptide of human GP88 used to develop
; OTHER INFORMATION: Neutralizing anti-human GP88 monoclonal antibody.
US-10-281-160-7

Alignment Scores:
Pred. No.: 0.000925 Length: 14
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-10-281-160-7 (1-14)

QY 1708 GCACGAGGGTACCAAGTGTTCGCGAGGAGGCCCGCGC 1749
Db 1 AlaArgArgGlyThrLysCysLeuArgArgGluAlaProArg 14
|||||

RESULT 4

US-09-813-156-7
; Sequence 7, Application US/09813156
; Patent No. US20020061859A1
; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: Z9996.488/P001-A
; CURRENT APPLICATION NUMBER: US/09/813,156
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 08/991,862
; PRIOR FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Human granulin
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)-(14)
; OTHER INFORMATION: Internal peptide of human GP88 used to develop
; OTHER INFORMATION: Neutralizing anti-human GP88 monoclonal antibody.
US-09-813-156-7

Alignment Scores:

Pred. No.: 0.000925 Length: 14
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 10 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-813-156-7 (1-14)

QY 1708 GCACGAGGGTACCAAGTGTTCGCGAGGAGGCCCGCGC 1749
Db 1 AlaArgArgGlyThrLysCysLeuArgArgGluAlaProArg 14
|||||

RESULT 5

US-09-824-807-7
; Sequence 7, Application US/09824807
; Patent No. US20020094966A1
; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: Z9996.488/P001-A
; CURRENT APPLICATION NUMBER: US/09/824,807
; CURRENT FILING DATE: 2001-04-04

;; PRIOR APPLICATION NUMBER: 08/991,862
;; PRIOR FILING DATE: 1997-12-16
;; PRIOR APPLICATION NUMBER: 08/863,862
;; PRIOR FILING DATE: 1997-05-23
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 7
;; LENGTH: 14
;; TYPE: PRT
;; ORGANISM: Human granulin
;; FEATURE:
;; NAME/KEY: PEPTIDE
;; LOCATION: (1)..(14)
;; OTHER INFORMATION: Internal peptide of human GP88 used to develop
;; neutralizing anti-human GP88 monoclonal antibody.

US-09-824-807-7

Alignment Scores:
Pred. No.: 0.000925 Length: 14
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 10 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-824-807-7 (1-14)

QY 1708 GCACGCGAGGTACCAAGTGTTCGCGAGGAGCCCGCGC 1749

Db 1 AlaArgGlyThrLysCysLeuArgGluAlaProArg 14

RESULT 6

US-09-826-290-195
;; Sequence 195, Application US/09826290
;; Patent No. US20020164668A1

GENERAL INFORMATION:

;; APPLICANT: Durham, L. Kathryn
;; APPLICANT: Friedman, David L.
;; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
;; APPLICANT: Kimmel, Lida H.
;; APPLICANT: Parekh, Rajesh Bhikhu
;; APPLICANT: Potter, David M.
;; APPLICANT: Rohlf, Christian
;; APPLICANT: Silber, B. Michael
;; APPLICANT: Stiger, Thomas R.
;; APPLICANT: Sunderland, P. Trey
;; APPLICANT: Townsend, Robert Reid
;; APPLICANT: White, Frost

;; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and

;; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of

;; FILE REFERENCE: 2572-1-001 N2

;; CURRENT APPLICATION NUMBER: US/09/826,290

;; CURRENT FILING DATE: 2001-04-30

;; PRIOR APPLICATION NUMBER: US 60/194,504

;; PRIOR FILING DATE: 2000-04-03

;; PRIOR APPLICATION NUMBER: US 60/253,647

;; PRIOR FILING DATE: 2000-11-28

;; NUMBER OF SEQ ID NOS: 492

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 195

;; LENGTH: 14

;; TYPE: PRT

;; ORGANISM: homo sapien

US-09-826-290-195

Alignment Scores:
Pred. No.: 2.44e+03 Length: 14
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.01% Indels: 0

DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-826-290-195 (1-14)

QY 1009 GGTACCTGTGAACAGGGGCC 1029

Db 1 GlyThrCysGluGlnGlyPro 7

RESULT 7

US-09-824-647-5

;; Sequence 5, Application US/09824647

;; Publication No. US20020183270A1

GENERAL INFORMATION:

;; APPLICANT: Seitero, Ginette

;; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS

;; FILE REFERENCE: 29996.488/P001-A

;; CURRENT APPLICATION NUMBER: US/09/824,647

;; CURRENT FILING DATE: 2001-04-04

;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,862

;; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17

;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/863,862

;; PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23

;; NUMBER OF SEQ ID NOS: 17

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 5

;; LENGTH: 14

;; TYPE: PRT

;; ORGANISM: mouse granulin

;; FEATURE:

;; NAME/KEY: PEPTIDE

;; LOCATION: (1)..(14)

;; OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the

;; OTHER INFORMATION: antisera against the GP88 used in the

;; OTHER INFORMATION: immunoaffinity step.

US-09-824-647-5

Alignment Scores:

Pred. No.: 2.44e+03 Length: 14
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.01% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-824-647-5 (1-14)

QY 1714 AGGGTACCAAGTGTTCGCGC 1734

Db 3 ArgGlyThrLysCysLeuArg 9

RESULT 8

US-10-218-509-5

;; Sequence 5, Application US/10218509

;; Publication No. US20030092661A1

GENERAL INFORMATION:

;; APPLICANT: Seitero, Ginette

;; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS

;; FILE REFERENCE: 29996.488/P001-A

;; CURRENT APPLICATION NUMBER: US/10/218,509

;; CURRENT FILING DATE: 2002-08-15

;; PRIOR APPLICATION NUMBER: 08/991,862

;; PRIOR FILING DATE: 1998-08-17

;; PRIOR APPLICATION NUMBER: 08/863,862

;; PRIOR FILING DATE: 1997-05-23

;; NUMBER OF SEQ ID NOS: 17

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 5

;; LENGTH: 14

;; TYPE: PRT

;; ORGANISM: mouse granulin

;; FEATURE:

;; NAME/KEY: PEPTIDE

;; LOCATION: (1)..(14)

OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the
OTHER INFORMATION: antisera against the GP88 used in the
OTHER INFORMATION: Immunofluorescence step.

US-10-218-509-5

Alignment Scores:
Pred. No.: 2.44e+03 14
Score: 7.00 7
Percent Similarity: 100.00% 0
Best Local Similarity: 100.00% 0
Query Match: 1.01% 0
DB: 9 0
Gaps: 0

US-09-824-647-16 (1-2095) x US-10-218-509-5 (1-14)

QY 1714 AGGGTACCAGTGTTCGCG 1734
DB 3 ArgGlyThrLysCysLeuArg 9

RESULT 9

US-10-281-160-5
Sequence 5, Application US/10281160
Publication No. US20030108950A1
GENERAL INFORMATION:
APPLICANT: Seriero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/10/281.160
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: US/08/991.862
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 08/863,862
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 14
TYPE: PRT
ORGANISM: mouse granulosa
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(14)
OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the
OTHER INFORMATION: antisera against the GP88 used in the
OTHER INFORMATION: Immunofluorescence step.

US-10-281-160-5

Alignment Scores:
Pred. No.: 2.44e+03 14
Score: 7.00 7
Percent Similarity: 100.00% 0
Best Local Similarity: 100.00% 0
Query Match: 1.01% 0
DB: 9 0
Gaps: 0

US-09-824-647-16 (1-2095) x US-10-281-160-5 (1-14)

QY 1714 AGGGTACCAGTGTTCGCG 1734
DB 3 ArgGlyThrLysCysLeuArg 9

RESULT 10

US-09-813-156-5
Sequence 5, Application US/09813156
Patent No. US20020061859A1
GENERAL INFORMATION:
APPLICANT: Seriero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/09/813.156
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1997-12-16

PRIOR APPLICATION NUMBER: 08/863,862
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5

LENGTH: 14
TYPE: PRT
ORGANISM: mouse granulosa
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(14)
OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the
OTHER INFORMATION: antisera against the GP88 used in the
OTHER INFORMATION: Immunofluorescence step.

US-09-813-156-5

Alignment Scores:
Pred. No.: 2.44e+03 14
Score: 7.00 7
Percent Similarity: 100.00% 0
Best Local Similarity: 100.00% 0
Query Match: 1.01% 0
DB: 10 0
Gaps: 0

US-09-824-647-16 (1-2095) x US-09-813-156-5 (1-14)

QY 1714 AGGGTACCAGTGTTCGCG 1734
DB 3 ArgGlyThrLysCysLeuArg 9

RESULT 11

US-09-824-807-5
Sequence 5, Application US/09824807
Patent No. US20020094966A1
GENERAL INFORMATION:
APPLICANT: Seriero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/09/824,807
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 08/863,862
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 14
TYPE: PRT
ORGANISM: mouse granulosa
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(14)
OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the
OTHER INFORMATION: antisera against the GP88 used in the
OTHER INFORMATION: Immunofluorescence step.

US-09-824-807-5

Alignment Scores:
Pred. No.: 2.44e+03 14
Score: 7.00 7
Percent Similarity: 100.00% 0
Best Local Similarity: 100.00% 0
Query Match: 1.01% 0
DB: 10 0
Gaps: 0

US-09-824-647-16 (1-2095) x US-09-824-807-5 (1-14)

QY 1714 AGGGTACCAGTGTTCGCG 1734
DB 3 ArgGlyThrLysCysLeuArg 9

RESULT 12

US-09-865-548A-108
; Sequence 108, Application US/09865548A
; Publication No. US20030096298A1

GENERAL INFORMATION:

; APPLICANT: Barnea, Elion
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar

; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULES

; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A

; CURRENT FILING DATE: 2001-05-16

; PRIOR APPLICATION NUMBER: US 60/290,958

; NUMBER OF SEQ ID NOS: 204

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 108

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: synthetic peptide

US-09-865-548A-108

Alignment Scores:
Pred. No.: 2.55e+07 Length: 9
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-865-548A-108 (1-9)

QY 459 CTGCCCCCAGCCCGGC 476

DB 3 LeuProHisAlaProgly 8

RESULT 13

US-10-254-446A-143

; Sequence 143, Application US/10254446A

; Publication No. US20030113714A1

GENERAL INFORMATION:

; APPLICANT: Belcher, Angela M

; APPLICANT: Smalley, Richard E.

; APPLICANT: Ryan, Esther

; APPLICANT: Lee, Seung-Wuk

; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES

; FILE REFERENCE: 119927-1066

; CURRENT APPLICATION NUMBER: US/10/254,446A

; CURRENT FILING DATE: 2003-02-19

; PRIOR APPLICATION NUMBER: 60/325,664

; PRIOR FILING DATE: 2001-09-28

; NUMBER OF SEQ ID NOS: 245

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 143

; LENGTH: 9

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: peptide with peptide binding sequence retrieved from phage biopar

US-10-254-446A-143

Alignment Scores:
Pred. No.: 2.55e+07 Length: 9
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-10-254-446A-143 (1-9)

QY 1638 CTGCTGTCCCTACGCCCA 1655

DB 2 LeuLeuSerLeuArgPro 7

RESULT 14

US-09-790-148-5

; Sequence 5, Application US/09790148

; Patent No. US20020001857A1

GENERAL INFORMATION:

; APPLICANT: VANDERMEEREN, MARC;

; MERCKEN, MARC;

; VANNECHELEN, EUGENE;

; VAN DE VOORDE, ANDRE

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES

; DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED

; PROTEIN TAU, HYBRIDOMAS SECRETING THESE

; ANTIBODIES, ANTIGEN RECOGNITION BY THESE

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BIERMAN & MUSERLIAN

; STREET: 600 THIRD AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10016

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/790,148

; FILING DATE: 21-Feb-2001

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: <Unknown>

; FILING DATE: 27-JUN-1994

; APPLICATION NUMBER: 08/256,167

; FILING DATE: 13-JUN-1994

; APPLICATION NUMBER: 08/244,951

; FILING DATE: 10-DEC-1993

; APPLICATION NUMBER: PCT/EP93/03499

; FILING DATE: 14-DEC-1992

; APPLICATION NUMBER: EP/92/403403.6

; FILING DATE: 14-DEC-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: CHARLES A. MUSERLIAN

; REGISTRATION NUMBER: 19,683

; REFERENCE/DOCKET NUMBER: 410.003-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 661-8000

; TELEFAX: (212) 661-8002

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9

; TYPE: Amino Acid

; STRANDEDNESS: Unknown

; TOPOLOGY: Unknown

; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-790-148-5

Alignment Scores:
Pred. No.: 2.55e+07 Length: 9
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.87% Indels: 0
DB: 10 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-790-148-5 (1-9)

QY 465 GGGGAGCAGCCCGCAGGA 448

DB 11

Db 1 GlyAlaAlaProProGly 6

RESULT 15

US-09-731-449-55
; Sequence 55, Application US/09731449
; Patent No. US2002015526A1
; GENERAL INFORMATION:

; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL SECRETED IMMUNOMODULATORY PROTEINS AND USES THEREOF
; FILE REFERENCE: 07334-320001
; CURRENT APPLICATION NUMBER: US/09/731,449
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/410,350
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 09/163,523
; PRIOR FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 62

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Fusion protein

US-09-731-449-55

Alignment Scores:

Pred. No.:	2.11e+04	Length:	10
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	0.86%	Indels:	0
DB:	9	Gaps:	0

US-09-824-647-16 (1-2095) x US-09-731-449-55 (1-10)

QY 112 CCCGAGGAGCCAGCTAC 129

Db 3 ProglyAlaSerTyr 8
|||||

RESULT 16

US-09-572-404B-375
; Sequence 375, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 375

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapiens

; FEATURE:

; OTHER INFORMATION: sequence located in NPR3 OR ANPRC at 33-42 and may interact with

US-09-572-404B-375

Alignment Scores:

Pred. No.:	2.11e+04	Length:	10
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	0.87%	Indels:	0
DB:	9	Gaps:	0

US-09-824-647-16 (1-2095) x US-09-572-404B-375 (1-10)

QY 1146 GCAGGTATCGGAGG 1129

|||||

Db 4 AlaGlyIleGlyGly 9

RESULT 17

US-09-572-404B-379
; Sequence 379, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 379

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapiens

; FEATURE:

; OTHER INFORMATION: sequence located in NPR3 OR ANPRC at 33-42 and may interact
; OTHER INFORMATION: Sequence 380 in this patent.

US-09-572-404B-379

Alignment Scores:

Pred. No.:	2.11e+04	Length:	10
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	0.87%	Indels:	0
DB:	9	Gaps:	0

US-09-824-647-16 (1-2095) x US-09-572-404B-379 (1-10)

QY 1146 GCAGGTATCGGAGG 1129

Db 4 AlaGlyIleGlyGly 9
|||||

RESULT 18

US-09-572-404B-389
; Sequence 389, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 389

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapiens

; FEATURE:

; OTHER INFORMATION: sequence located in NPR3 OR ANPRC at 34-43 and may interact
; OTHER INFORMATION: Sequence 390 in this patent.

US-09-572-404B-389

Alignment Scores:

Pred. No.:	2.11e+04	Length:	10
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	0.87%	Indels:	0
DB:	9	Gaps:	0

US-09-824-647-16 (1-2095) x US-09-572-404B-389 (1-10)

QY 1146 GCAGGTATCGGAGG 1129

Db 3 AlaGlyIleGlyGly 8
|||||

RESULT 19

```
US-09-572-404B-403
; Sequence 403, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 403
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in NPR3 OR ANPRC at 33-42 and may interact with
; OTHER INFORMATION: Sequence 404 in this patent.
US-09-572-404B-403

Alignment Scores:
Pred. No.: 2.11e+04 Length: 10
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.87% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-572-404B-403 (1-10)

QY 1146 GCAGGTATCGGAGGAGG 1129
Db 4 AlaGlylleGlyGlyGly 9

RESULT 20
US-09-572-404B-409
; Sequence 409, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 409
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in NPR3 OR ANPRC at 33-42 and may interact with
; OTHER INFORMATION: Sequence 410 in this patent.
US-09-572-404B-409

Alignment Scores:
Pred. No.: 2.11e+04 Length: 10
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.87% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-572-404B-409 (1-10)

QY 1146 GCAGGTATCGGAGGAGG 1129
Db 4 AlaGlylleGlyGlyGly 9

RESULT 21
US-09-572-404B-415
; Sequence 415, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 415
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in NPR3 OR ANPRC at 33-42 and may interact with
; OTHER INFORMATION: Sequence 416 in this patent.
US-09-572-404B-415

Alignment Scores:
Pred. No.: 2.11e+04 Length: 10
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.87% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-572-404B-415 (1-10)

QY 1146 GCAGGTATCGGAGGAGG 1129
Db 4 AlaGlylleGlyGlyGly 9

RESULT 22
US-09-572-404B-419
; Sequence 419, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 419
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in NPR3 OR ANPRC at 33-42 and may interact with
; OTHER INFORMATION: Sequence 420 in this patent.
US-09-572-404B-419

Alignment Scores:
Pred. No.: 2.11e+04 Length: 10
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.87% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-572-404B-419 (1-10)

QY 1146 GCAGGTATCGGAGGAGG 1129
Db 4 AlaGlylleGlyGlyGly 9

RESULT 23
US-09-572-404B-500
; Sequence 500, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
```

; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 500
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in PTHR1 OR PTHR at 271-280 and may interact with
; OTHER INFORMATION: Sequence 499 in this patent.
US-09-572-404B-500

Alignment Scores:
Pred. No.: 2.11e+04 Length: 10
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-572-404B-500 (1-10)

QY 122 CCAGCTACAGCTGCTGCC 139
DB 1 ProAlaThrAlaAlaAla 6

RESULT 24

US-09-572-404B-502
; Sequence 502, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 502
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in PTHR1 OR PTHR at 270-279 and may interact with
; OTHER INFORMATION: Sequence 501 in this patent.
US-09-572-404B-502

Alignment Scores:
Pred. No.: 2.11e+04 Length: 10
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-572-404B-502 (1-10)

QY 122 CCAGCTACAGCTGCTGCC 139
DB 2 ProAlaThrAlaAlaAla 7

RESULT 25

US-09-572-404B-1060
; Sequence 1060, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 2101

; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 1060
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in ITPKB at 1964-1973 and may interact with
; OTHER INFORMATION: 1059 in this patent.
US-09-572-404B-1060

Alignment Scores:
Pred. No.: 2.11e+04 Length: 10
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-572-404B-1060 (1-10)

QY 915 GGGGCGCTGGGCTGCTG 932
DB 5 GlyGlyLeuGlyLeuLeu 10

RESULT 26

US-09-572-404B-2096
; Sequence 2096, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 2096
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in SG2NA at 48-57 and may interact with Seq
; OTHER INFORMATION: in this patent.
US-09-572-404B-2096

Alignment Scores:
Pred. No.: 2.11e+04 Length: 10
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-572-404B-2096 (1-10)

QY 1397 GGAGCTGGGCTGCTGCC 1414
DB 1 GlyAlaGlyProAlaAla 6

RESULT 27

US-09-572-404B-2101
; Sequence 2101, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 2101

;
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in CNTFR at 323-332 and may interact with Sequence 2773 in t
; OTHER INFORMATION: in this patent.
US-09-572-404B-2101

Alignment Scores:
Pred. No.: 2.11e+04 Length: 10
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-572-404B-2101 (1-10)

QY 1859 TCCCTAGCACCTCCCCCT 1876
Db 3 SerLeuAlaProPro 8
|||||

RESULT 28
US-09-572-404B-2103
; Sequence 2103, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 2103
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in CNTFR at 322-331 and may interact with Sequence 2773 in t
; OTHER INFORMATION: in this patent.
US-09-572-404B-2103

Alignment Scores:
Pred. No.: 2.11e+04 Length: 10
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-572-404B-2103 (1-10)

QY 1859 TCCCTAGCACCTCCCCCT 1876
Db 4 SerLeuAlaProPro 9
|||||

RESULT 29
US-09-572-404B-2773
; Sequence 2773, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 2773
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in CNTFR at 88-97 and may interact w

;
; FEATURE:
; OTHER INFORMATION: sequence located in GUCY2D OR GUC2D OR RETGC1 OR RETGC OR
; OTHER INFORMATION: CORD6 at 713-722 and may interact with Sequence 2774 in t
US-09-572-404B-2773

Alignment Scores:
Pred. No.: 2.11e+04 Length: 10
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-572-404B-2773 (1-10)

QY 1762 TTGAGGCGCCGCTGCTTG 1779
Db 2 LeuArgAspProAlaLeu 7
|||||

RESULT 30
US-09-572-404B-3064
; Sequence 3064, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3064
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in DD1R1 OR GADD45 at 104-113 and may in
; OTHER INFORMATION: Sequence 3063 in this patent.
US-09-572-404B-3064

Alignment Scores:
Pred. No.: 2.11e+04 Length: 10
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-572-404B-3064 (1-10)

QY 1400 GCTGGCGCTGCTGCCAGT 1417
Db 5 AlaGlyProAlaAlaSer 10
|||||

RESULT 31
US-09-572-404B-3256
; Sequence 3256, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3256
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in OXT OR OT at 88-97 and may interact w

US-09-572-404B-3256

Alignment Scores:
 Pred. No.: 2.11e+04 Length: 10
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.87% Indels: 0
 DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-572-404B-3256 (1-10)

QY 1091 AAGCTTGTGGTCTGGC 1074
 |||||
 Db 3 Lysalacysglysergly 8

RESULT 32

US-09-572-404B-3258
 ; Sequence 3258, Application US/09572404B
 ; Publication No. US20030078374A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Proteom Ltd
 ; TITLE OF INVENTION: Complementary peptide ligands from the human genome
 ; FILE REFERENCE: Human patent
 ; CURRENT APPLICATION NUMBER: US/09/572,404B
 ; CURRENT FILING DATE: 2000-05-17
 ; NUMBER OF SEQ ID NOS: 4203
 ; SOFTWARE: ProtPatent version 1.0
 ; SEQ ID NO 3258
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; OTHER INFORMATION: sequence located in OXT OR OT at 87-96 and may interact with Sequ
 ; OTHER INFORMATION: sequence 3257 in this patent.

US-09-572-404B-3258

Alignment Scores:
 Pred. No.: 2.11e+04 Length: 10
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.87% Indels: 0
 DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-572-404B-3258 (1-10)

QY 1091 AAGCTTGTGGTCTGGC 1074
 |||||
 Db 4 Lysalacysglysergly 9

RESULT 33

US-09-572-404B-3260
 ; Sequence 3260, Application US/09572404B
 ; Publication No. US20030078374A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Proteom Ltd
 ; TITLE OF INVENTION: Complementary peptide ligands from the human genome
 ; FILE REFERENCE: Human patent
 ; CURRENT APPLICATION NUMBER: US/09/572,404B
 ; CURRENT FILING DATE: 2000-05-17
 ; NUMBER OF SEQ ID NOS: 4203
 ; SOFTWARE: ProtPatent version 1.0
 ; SEQ ID NO 3260
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; OTHER INFORMATION: sequence located in AVP OR ARVP OR VP at 88-97 and may interact
 ; OTHER INFORMATION: Sequence 3259 in this patent.

US-09-572-404B-3260

Alignment Scores:

Pred. No.: 2.11e+04 Length: 10
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.87% Indels: 0
 DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-572-404B-3260 (1-10)

QY 1091 AAGCTTGTGGTCTGGC 1074
 |||||
 Db 3 Lysalacysglysergly 8

RESULT 34

US-09-572-404B-3262
 ; Sequence 3262, Application US/09572404B
 ; Publication No. US20030078374A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Proteom Ltd
 ; TITLE OF INVENTION: Complementary peptide ligands from the human genome
 ; FILE REFERENCE: Human patent
 ; CURRENT APPLICATION NUMBER: US/09/572,404B
 ; CURRENT FILING DATE: 2000-05-17
 ; NUMBER OF SEQ ID NOS: 4203
 ; SOFTWARE: ProtPatent version 1.0
 ; SEQ ID NO 3262
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; OTHER INFORMATION: sequence located in AVP OR ARVP OR VP at 87-96 and may inter
 ; OTHER INFORMATION: Sequence 3261 in this patent.

US-09-572-404B-3262

Alignment Scores:
 Pred. No.: 2.11e+04 Length: 10
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.87% Indels: 0
 DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-572-404B-3262 (1-10)

QY 1091 AAGCTTGTGGTCTGGC 1074
 |||||
 Db 4 Lysalacysglysergly 9

RESULT 35

US-09-572-404B-3586
 ; Sequence 3586, Application US/09572404B
 ; Publication No. US20030078374A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Proteom Ltd
 ; TITLE OF INVENTION: Complementary peptide ligands from the human genome
 ; FILE REFERENCE: Human patent
 ; CURRENT APPLICATION NUMBER: US/09/572,404B
 ; CURRENT FILING DATE: 2000-05-17
 ; NUMBER OF SEQ ID NOS: 4203
 ; SOFTWARE: ProtPatent version 1.0
 ; SEQ ID NO 3586
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; OTHER INFORMATION: sequence located in PRD1 at 316-325 and may interact with S
 ; OTHER INFORMATION: In this patent.

US-09-572-404B-3586

Alignment Scores:
 Pred. No.: 2.11e+04 Length: 10
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-572-404B-3586 (1-10)

QY 1400 GCTGGCCTGTGCCAGT 1417

DB 2 AlaGlyProAlaAlaSer 7

RESULT 36

US-09-572-404B-3672

; Sequence 3672, Application US/09572404B

; Publication No. US20030078374A1

; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands from the human genome

; FILE REFERENCE: Human patent

; CURRENT APPLICATION NUMBER: US/09/572,404B

; CURRENT FILING DATE: 2000-05-17

; NUMBER OF SEQ ID NOS: 4203

; SOFTWARE: ProtPatent version 1.0

; SEQ ID NO 3672

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapiens

; FEATURE:

; OTHER INFORMATION: sequence located in Unknown at 95-104 and may interact with Sequence

; OTHER INFORMATION: 3673 in this patent.

US-09-572-404B-3672

Alignment Scores:

Pred. No.: 2.11e+04

Score: 6.00 Length: 10

Percent Similarity: 100.00% Matches: 6

Best Local Similarity: 100.00% Conservative: 0

Query Match: 0.87% Mismatches: 0

DB: 9 Indels: 0

Gaps: 0

US-09-824-647-16 (1-2095) x US-09-572-404B-3672 (1-10)

QY 1042 AGGCACCTGTGGGCC 1025

DB 3 ArgAlaProGlyGlyAla 8

RESULT 37

US-09-572-404B-3673

; Sequence 3673, Application US/09572404B

; Publication No. US20030078374A1

; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands from the human genome

; FILE REFERENCE: Human patent

; CURRENT APPLICATION NUMBER: US/09/572,404B

; CURRENT FILING DATE: 2000-05-17

; NUMBER OF SEQ ID NOS: 4203

; SOFTWARE: ProtPatent version 1.0

; SEQ ID NO 3673

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapiens

; FEATURE:

; OTHER INFORMATION: sequence located in Unknown at 95-104 and may interact with Sequence

; OTHER INFORMATION: 3672 in this patent.

US-09-572-404B-3673

Alignment Scores:

Pred. No.: 2.11e+04

Score: 6.00 Length: 10

Percent Similarity: 100.00% Matches: 6

Best Local Similarity: 100.00% Conservative: 0

Query Match: 0.87% Mismatches: 0

DB: 9 Indels: 0

Gaps: 0

US-09-824-647-16 (1-2095) x US-09-572-404B-3673 (1-10)

QY 1042 AGGCACCTGTGGGCC 1025

DB 3 ArgAlaProGlyGlyAla 8

RESULT 38

US-09-572-404B-3674

; Sequence 3674, Application US/09572404B

; Publication No. US20030078374A1

; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands from the human genome

; FILE REFERENCE: Human patent

; CURRENT APPLICATION NUMBER: US/09/572,404B

; CURRENT FILING DATE: 2000-05-17

; NUMBER OF SEQ ID NOS: 4203

; SOFTWARE: ProtPatent version 1.0

; SEQ ID NO 3674

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapiens

; FEATURE:

; OTHER INFORMATION: sequence located in Unknown at 96-105 and may interact with

; OTHER INFORMATION: 3675 in this patent.

US-09-572-404B-3674

Alignment Scores:

Pred. No.: 2.11e+04

Score: 6.00 Length: 10

Percent Similarity: 100.00% Matches: 6

Best Local Similarity: 100.00% Conservative: 0

Query Match: 0.87% Mismatches: 0

DB: 9 Indels: 0

Gaps: 0

US-09-824-647-16 (1-2095) x US-09-572-404B-3674 (1-10)

QY 1042 AGGCACCTGTGGGCC 1025

DB 2 ArgAlaProGlyGlyAla 7

RESULT 39

US-09-572-404B-3675

; Sequence 3675, Application US/09572404B

; Publication No. US20030078374A1

; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands from the human genome

; FILE REFERENCE: Human patent

; CURRENT APPLICATION NUMBER: US/09/572,404B

; CURRENT FILING DATE: 2000-05-17

; NUMBER OF SEQ ID NOS: 4203

; SOFTWARE: ProtPatent version 1.0

; SEQ ID NO 3675

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapiens

; FEATURE:

; OTHER INFORMATION: sequence located in Unknown at 94-103 and may interact with

; OTHER INFORMATION: 3674 in this patent.

US-09-572-404B-3675

Alignment Scores:

Pred. No.: 2.11e+04

Score: 6.00 Length: 10

Percent Similarity: 100.00% Matches: 6

Best Local Similarity: 100.00% Conservative: 0

Query Match: 0.87% Mismatches: 0

DB: 9 Indels: 0

Gaps: 0

US-09-824-647-16 (1-2095) x US-09-572-404B-3675 (1-10)

OY 1042 AGGCACCTGTGGGSCC 1025
Db ||||||||||||||||
4 ArgAlaProGlyGlyAla 9

RESULT 40

US-09-572-404B-3688
; Sequence 3688, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3688
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in ATP5A1 at 456-465 and may interact with Sequence 3689 in this patent.
US-09-572-404B-3688

Alignment Scores:
Pred. No.: 2.11e+04 Length: 10
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-572-404B-3688 (1-10)

OY 972 CTGCTCCCGCGGGGTT 989
Db ||||||||||||||||
5 LeuLeuSerArgGlyVal 10

RESULT 41

US-09-572-404B-3850
; Sequence 3850, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3850
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in CCKBR OR CCKRB at 310-319 and may interact with Sequence 3851 in this patent.
US-09-572-404B-3850

Alignment Scores:
Pred. No.: 2.11e+04 Length: 10
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.87% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-572-404B-3850 (1-10)

OY 1393 CCTGGCTCGGCAGCAGG 1376
Db ||||||||||||||||
5 ProGlySerGlySerArg 10

RESULT 42

US-09-572-404B-3851
; Sequence 3851, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3851
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in CCKBR OR CCKRB at 310-319 and may interact with Sequence 3850 in this patent.
US-09-572-404B-3851

Alignment Scores:
Pred. No.: 2.11e+04 Length: 10
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.87% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-572-404B-3851 (1-10)

OY 1393 CCTGGCTCGGCAGCAGG 1376
Db ||||||||||||||||
5 ProGlySerGlySerArg 10

RESULT 43

US-09-789-649-27
; Sequence 27, Application US/09789649
; Publication No. US20030082804A1
; GENERAL INFORMATION:
; APPLICANT: Valmori, Danila
; APPLICANT: Cerottini, Jean-Charles
; APPLICANT: Romero, Pedro
; TITLE OF INVENTION: Isolated No. US20030082804A1 - And Decapeptides Which Bind To HLA Molecules, and the Use Thereof
; FILE REFERENCE: LUD 5483.2
; CURRENT APPLICATION NUMBER: US/09/789,649
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US09/099,543
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: US 09/061,388
; PRIOR FILING DATE: 1998-04-16
; PRIOR APPLICATION NUMBER: US 08/880,963
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 27
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derivative of SEQ ID NO:1
US-09-789-649-27

Alignment Scores:
Pred. No.: 2.11e+04 Length: 10
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.87% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-09-789-649-27 (1-10)

QY 903 GCAGCAGGTATAGCATC 886
|||||
Db 2 AlaAlaGlyIleAlaIle 7

RESULT 44

US-10-254-426-55
; Sequence 55, Application US/10254426
; Publication No. US20030113865A1
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL SECRETED IMMUNOMODULATORY PROTEINS AND USES THEREOF
; FILE REFERENCE: 07334-320001
; CURRENT APPLICATION NUMBER: US/10/254,426
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US/09/731,449
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/410,350
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 09/163,523
; PRIOR FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fuslon protein
US-10-254-426-55

Alignment Scores:
Pred. No.: 2.11e+04 Length: 10
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-10-254-426-55 (1-10)

QY 112 CCCGAGGAGCCAGCTAC 129
|||||
Db 3 ProGlyGlyAlaSerTyr 8

RESULT 45

US-10-216-122-80
; Sequence 80, Application US/10216122
; Publication No. US20030121063A1
; GENERAL INFORMATION:
; APPLICANT: Kazazian, Haig H.
; APPLICANT: Ostertag, Eric
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF MAMMALIAN RETROTRANSPOSONS
; FILE REFERENCE: 053893-5006-03
; CURRENT APPLICATION NUMBER: US/10/216,122
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 09/653,812
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 08/847,844
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: US 08/749,805
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: US 60/006,831
; PRIOR FILING DATE: 1995-11-16
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-122-80

Alignment Scores:
Pred. No.: 2.11e+04 Length: 10
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.86% Indels: 0
DB: 9 Gaps: 0

US-09-824-647-16 (1-2095) x US-10-216-122-80 (1-10)

QY 1164 GGAGTGGGCTGCTGTCC 1181
|||||
Db 4 GlyValGlyLeuLeuSer 9

Search completed: July 7, 2003, 16:14:55
Job time : 81 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: July 7, 2003, 16:02:12 ; Search time 76.5 Seconds
(without alignments)
5265.402 Million cell updates/sec

Title: US-09-824-647-16

Perfect score: 694

Sequence: 1 cgcagcgaccatgtggac.....ataaagttgtcactttctt 2095

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283224 seqs, 96134422 residues

Word size: 1

Total number of hits satisfying chosen parameters: 4128

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-Q/cqg2_1/USPTO.spool/US09824647/runat_07072003_154759_26625/app_query.fasta_1.2247
-DB=PIR_73 -OPT=fastan -SUFFIX=lim.rpr -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-NORMALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=45 -MODE=LOCAL -OUTFMT=ptp
-NOR-ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=15
-USER=US09824647 -ECGN_1_1_108 -runat_07072003_154759_26625 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	0.9	11	2 PU0034	dextranucrase (EC
2	6	0.9	12	2 A29169	phospholipase A2 (
3	6	0.9	14	2 B60683	malate dehydrogena
4	6	0.9	15	2 S70719	H+-transporting tw
5	5	0.7	8	2 A23967	leucopyrokinin - M
6	5	0.7	8	4 I55411	hypothetical histo
7	5	0.7	9	1 YFPG	thymic factor - pi
8	5	0.7	9	2 A60957	thymocyte growth p
9	5	0.7	9	2 A31576	xylose isomerase (
10	5	0.7	9	2 A60427	macrophage cytoox
11	5	0.7	10	2 S39392	calpain (EC 3.4.22
12	5	0.7	11	2 A34662	Achatina cardio-ex
13	5	0.7	11	2 PH1632	Ig H chain V-D-J r
14	5	0.7	11	4 I54081	retinoic acid rece

c 15	5	0.7	12	2 PN0162	malate dehydrogena
c 16	5	0.7	12	2 I39390	acetylcholine rece
c 17	5	0.7	12	2 PH1175	T-cell receptor al
c 18	5	0.7	12	2 A60528	insulin-like growt
c 19	5	0.7	12	2 S65626	phosphorylase b -
c 20	5	0.7	12	2 C30503	Ig gamma-2b chain
c 21	5	0.7	12	2 A33520	inhibitory diffus
c 22	5	0.7	12	2 A58370	microbin B17 - Esc
c 23	5	0.7	13	2 A32734	enkephalin precurs
c 24	5	0.7	13	2 G22565	R-phycoerythrin ga
c 25	5	0.7	13	2 PS0443	potassium channel
c 26	5	0.7	13	2 B61458	Ig kappa chain V-I
c 27	5	0.7	13	2 S47388	T-cell antigen rec
c 28	5	0.7	13	2 B61233	conceptus protein
c 29	5	0.7	13	2 B61233	conceptus protein
c 30	5	0.7	14	1 QMVHMM	mastoparan M - hor
c 31	5	0.7	14	2 B60683	malate dehydrogena
c 32	5	0.7	14	2 S23376	collagen alpha cha
c 33	5	0.7	14	2 PH1763	T cell receptor al
c 34	5	0.7	14	2 PH1767	T cell receptor al
c 35	5	0.7	14	2 S57574	T cell receptor V-
c 36	5	0.7	14	2 JH0516	insulin-like growt
c 37	5	0.7	14	2 JH0516	insulin-like growt
c 38	5	0.7	14	2 PH1639	Ig H chain V-D-J r
c 39	5	0.7	14	2 PH1597	Ig H chain V-D-J r
c 40	5	0.7	14	2 D35141	T-cell receptor de
c 41	5	0.7	15	1 LFTWL	leu leader peptide
c 42	5	0.7	15	2 I52734	gene c-Ki-ras prot
c 43	5	0.7	15	2 I49407	placental calcium-
c 44	5	0.7	15	2 PQ0545	capsid protein VP1
c 45	5	0.7	15	2 B35389	urease (EC 3.5.1.5

ALIGNMENTS

RESULT 1

PU0034
dextranucrase (EC 2.4.1.5) - Streptococcus bovis (fragment)
C:Species: Streptococcus bovis
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 18-Sep-1996
C:Accession: PU0034
R:Uezono, Y.; Tsumori, H.; Mukasa, H.
submitted to JIPID, October 1993
A:Description: Purification and properties of glucosyltransferase synthesizing 1
A:Reference number: PU0034
A:Accession: PU0034
A:Molecule type: protein
A:Residues: 1-11 <UEZ>
A:Experimental source: ATCC 9809
C:Keywords: glycosyltransferase; hexosyltransferase

Alignment Scores:
Pred. No.: 1.17e+04
Score: 6.00
Length: 11
Matches: 6
Conservative: 0
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 0.86%
Indels: 0
DB: 2
Gaps: 0

US-09-824-647-16 (1-2095) x PU0034 (1-11)

QY 1331 GAGACATCGCTGTGACC 1348

Db 2 GluThrSerAlaValThr 7

RESULT 2

A29169
phospholipase A2 (EC 3.1.1.4) precursor - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 31-Oct-1997
C:Accession: A29169
R:Duttlh, C.E.; Van Doren, P.J.; Verheul, F.E.A.M.; De Haas, G.H.
Eur. J. Biochem. 53, 91-97, 1975

A:Title: Isolation and properties of phospholipase A2 from ox and sheep pancreas.

A:Reference number: A94661

A:Accession: A29169

A:Molecule type: protein

A:Residues: 1-12 <OUT>

C:Superfamily: phospholipase A2

C:Keywords: carboxylic ester hydrolase; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Alignment Scores:

Pred. No.: 12
Length: 1.15e+04
Score: 6.00
Matches: 6
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 0.86%
Indels: 0
Gaps: 0
DB:

US-09-824-647-16 (1-2095) x A29169 (1-12)

OY 36 GGCCTTACAGCAGGCT 53

DB 3 GlyLeuAsnSerArgAla 8

RESULT 3

malate dehydrogenase (decarboxylating) (EC 1.1.1.39) - millet (fragment)

C:Species: Panicum sp. (millet)

C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 24-Feb-1994

C:Accession: B60683

R:Murata, T.; Ikeda, J.; Takano, M.; Ohsugi, R.

Plant Cell Physiol. 30, 429-437, 1989

A:Title: Comparative studies of NAD-malic enzyme from leaves of various C-4 plants.

A:Reference number: A60683

A:Accession: B60683

A:Molecule type: protein

A:Residues: 1-14 <MUR>

C:Keywords: oxidoreductase; photosynthesis

Alignment Scores:

Pred. No.: 14
Length: 1.13e+04
Score: 6.00
Matches: 6
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 0.87%
Indels: 0
Gaps: 0
DB:

US-09-824-647-16 (1-2095) x B60683 (1-14)

OY 462 GCAGCACCCCGAGGCC 445

DB 3 AlaAlaProGlyAla 8

RESULT 4

H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - Salmonella typhimurium (fr

C:Species: Salmonella typhimurium

C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 03-Jun-2002

C:Accession: S70719

R:Qi, S.Y.; Li, Y.; Szyroki, A.; Giles, I.G.; Moir, A.; O'Connor, C.D.

Mol. Microbiol. 17, 523-531, 1995

A:Title: Salmonella typhimurium responses to a bactericidal protein from human neutrophil

A:Reference number: S70719; MUID:96100451; PMID:8559071

A:Accession: S70719

A:Molecule type: protein

A:Residues: 1-15 <QIS>

A:Experimental source: strain SL1344

C:Keywords: ATP binding; hydrogen-ion transport; hydrolase

Alignment Scores:

Pred. No.: 15
Length: 1.12e+04
Score: 6.00
Matches: 6
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0

Query Match:

0.87%

Indels:

0

Gaps:

0

US-09-824-647-16 (1-2095) x S70719 (1-15)

OY 747 GTGCAGGTGATCGGAGCA 730

DB 6 ValGlnValIleGlyAla 11

RESULT 5

A23967

leucopyrokinin - Madeira cockroach

C:Species: Leucophaea maderae (Madeira cockroach)

C:Date: 31-Mar-1988 #sequence_revision 26-May-1994 #text_change 11-Jul-1997

C:Accession: A23967

R:Nachman, R.J.; Holman, G.M.; Cook, B.J.

Biochem. Biophys. Res. Commun. 137, 936-942, 1986

A:Title: Active fragments and analogs of the insect neuropeptide leucopyrokinin: st

A:Reference number: A23967; MUID:86269041; PMID:3015140

A:Accession: A23967

A:Molecule type: protein

A:Residues: 1-8 <NAC>

C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Leu) #status experimental

Alignment Scores:

Pred. No.: 8
Length: 2.4e+07
Score: 5.00
Matches: 5
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 0.73%
Indels: 0
Gaps: 0
DB:

US-09-824-647-16 (1-2095) x A23967 (1-8)

OY 1568 ACGTCCTTCACACC 1554

DB 2 ThrSerPheThrPro 6

RESULT 6

I55411

hypothetical histone H2A.X (mistranslated) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 28-Jan-2000

C:Accession: I55411

R:Ivanova, V.S.; Hatch, C.L.; Bonner, W.M.

J. Biol. Chem. 269, 24189-24194, 1994

A:Title: Characterization of the human histone H2A.X gene. Comparison of its promot

A:Reference number: I55411; MUID:95014156; PMID:7929075

A:Accession: I55411

A>Status: translation not shown; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-8 <IVA>

A:Cross-references: GB:S73863; NID:9765295; PIDN:AAI4141.1; PID:94261841

A>Note: this is a hypothetical translation of a sequence from the promoter region f

C:Genetics:

A:Gene: H2A.X

Alignment Scores:

Pred. No.: 8
Length: 2.4e+07
Score: 5.00
Matches: 5
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 0.72%
Indels: 0
Gaps: 0
DB:

US-09-824-647-16 (1-2095) x I55411 (1-8)

OY 1379 GGTGCGCGAGCCAGG 1393

DB 4 AlaAlaArgAlaArg 8

RESULT 7

YFPG
thymic factor - pig
N:Alternate names: FTS (facteur thymique serique)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 07-May-1999
C:Accession: A01523; A06983
R:Pleau, J.M.; Dardenne, M.; Blouquit, Y.; Bach, J.F.
J. Biol. Chem. 252, 8045-8047, 1977
A:Title: Structural study of circulating thymic factor: a peptide isolated from pig serum
A:Reference number: A01523; MUID:78026571; PMID:914862
A:Accession: A01523
A:Molecule type: protein
A:Residues: 1-9 <BLE>
R:Bach, J.F.; Dardenne, M.; Pleau, J.M.; Rosa, J.
Nature 266, 55-57, 1977
A:Title: Biochemical characterisation of a serum thymic factor.
A:Reference number: A06983; MUID:77123829; PMID:300146
A:Accession: A06983
A:Molecule type: protein
A:Residues: 'Z', 2-4, 'Z', 6-9 <BAC>
C:Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral
in a variety of immunoassays.
C:Comment: See PIR:A06957 (sheep) for discussion of another possible N-terminal modification
C:Superfamily: thymic factor
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Alignment Scores:
Pred. No.: 2.14e+07 Length: 9
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.73% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x YFPG (1-9)

QY 1387 AGCCAGGTGGGAGC 1401
|||||
Db 4 SerGlnGlySer 8

RESULT 8

A06957
thymocyte growth peptide - sheep
N:Contains: FTS (facteur thymique serique)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999
C:Accession: A06957
R:Ernstroem, U.; Gavvelin, G.; Rudja, J.M.
Biosci. Rep. 10, 403-412, 1990
A:Title: Purification of thymocyte growth peptide (TGP) from sheep thymus. Relationship
A:Reference number: A06957; MUID:91064427; PMID:2249004
A:Accession: A06957
A:Molecule type: protein
A:Residues: 1-9 <ERN>
C:Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral
in a variety of immunoassays.
C:Comment: This peptide was isolated in two forms. One form contained the pyrrolidone ca
r form (thymocyte growth peptide) contains a large, non-peptide blocking group with a hi
C:Superfamily: thymic factor
F:1/Modified site: pyrrolidone carboxylic acid (Glx) (In FTS) #status experimental
F:1/Modified site: blocked amino end (Glx) (In thymocyte growth peptide) #status experim

Alignment Scores:
Pred. No.: 2.14e+07 Length: 9
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.73% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x A60957 (1-9)

QY 1387 AGCCAGGTGGGAGC 1401
|||||
Db 4 SerGlnGlySer 8

RESULT 9

A31576
xylose isomerase (EC 5.3.1.5), intracellular - Streptomyces sp. (fragment)
C:Species: Streptomyces sp.
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 28-Apr-1993
C:Accession: A31576
R:Pawar, H.S.; Kannan, K.; Srinivasan, M.C.; Vartak, H.G.
Biochem. Biophys. Res. Commun. 155, 411-417, 1988
A:Title: Purification and characterisation of glucose (xylose) isomerase from Cha
A:Reference number: A31576; MUID:88326335; PMID:3415697
A:Contents: Chaetia sp. NCL 82-5-1
A:Accession: A31576
A:Molecule type: protein
A:Residues: 1-9 <PAW>
C:Keywords: intramolecular oxidoreductase; isomerase

Alignment Scores:
Pred. No.: 2.14e+07 Length: 9
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.73% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x A31576 (1-9)

QY 1380 GCAGGTCCGCCAC 1366
|||||
Db 3 AlaGlySerAlaHis 7

RESULT 10

A60427
macrophage cytotoxicity-inducing factor, 29K - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Jun-1993
C:Accession: A60427
R:Jones, C.M.; Prince, C.A.; Williams, J.S.
Exp. Hematol. 19, 704-709, 1991
A:Title: Purification and amino acid analysis of a human macrophage cytotoxicity-
A:Reference number: A60427; MUID:91372335; PMID:1909970
A:Accession: A60427
A:Molecule type: protein
A:Residues: 1-9 <JON>
A:Note: the sequence from the text on page 706 is inconsistent with that from pag
C:Keywords: cytokine

Alignment Scores:
Pred. No.: 2.14e+07 Length: 9
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.73% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x A60427 (1-9)

QY 1227 GGGCGAGCAGTGCTG 1213
|||||
Db 1 GlyAlaAlaValIeu 5

RESULT 11

S39392
calpain (EC 3.4.22.17) II light chain - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 18-Feb-1994 #sequence_revision 24-Jul-1998 #text_change 29-Sep-1999
C:Accession: S39392
R:Crawford, C.; Brown, N.R.; Willis, A.C.

Biochem. J. 296, 135-142, 1993
 A:Title: Studies of the active site of m-calpain and the interaction with calpastatin.
 A:Reference number: S39391; MUID:94071815; PMID:8250833
 A:Accession: S39392

A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <GRA>
 C:Superfamily: calpain small chain; calmodulin repeat homology
 C:Keywords: cysteine proteinase; EF hand; hydrolase

Alignment Scores:
 Pred. No.: 1.21e+05 Length: 10
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.73% Indels: 0
 DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x S39392 (1-10)

QY 828 AGTCAGGAGTCCGT 814
 DB 4 SerGluGluValArg 8
 |||||

RESULT 12

A34662
 Achatina cardio-excitatory peptide-1 - giant African snail
 C:Species: Achatina fulica (giant African snail)
 C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 11-Jul-1997
 C:Accession: A34662
 R:Fujimoto, K.; Ohta, N.; Yoshida, M.; Kubota, I.; Muneoka, Y.; Kobayashi, M.
 Biochem. Biophys. Res. Commun. 167, 777-783, 1990
 A:Title: A novel cardio-excitatory peptide isolated from the atria of the African giant
 A:Reference number: A34662; MUID:90211261; PMID:2322251
 A:Accession: A34662

A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-11 <PUV>
 C:Keywords: amidated carboxyl end
 F:11/Modified site: amidated carboxyl end (Phe) #status experimental

Alignment Scores:
 Pred. No.: 1.19e+05 Length: 11
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.73% Indels: 0
 DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x A34662 (1-11)

QY 100 AGGCCACAGGCAGA 86
 DB 6 ArgProGlnGlyArg 10
 |||||

RESULT 13

PH1632
 Ig H chain V-D-J region (clone B-less 209) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C:Accession: PH1632

R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A:Reference number: PH1580; MUID:93301609; PMID:8315387
 A:Accession: PH1632
 A:Molecule type: DNA
 A:Residues: 1-11 <LEV>
 A:Experimental source: bone marrow pre-B lymphocyte
 C:Keywords: immunoglobulin

Alignment Scores:
 Pred. No.: 1.19e+05 Length: 11

Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.72% Indels: 0
 DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x PH1632 (1-11)

QY 1705 TGGCAGCAGGCGGT 1719
 DB 1 CysAlaArgArgGly 5
 |||||

RESULT 14

I54081
 retinoic acid receptor alpha, exon 3 (mistranslated) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 28-Jun-1999
 C:Accession: I54081
 R:Dong, S.; Geng, J.P.; Tong, J.H.; Wu, Y.; Cai, J.R.; Sun, G.L.; Chen, S.R.; Wang,
 Genes Chromosomes Cancer 6, 133-139, 1993
 A:Title: Breakpoint clusters of the PML gene in acute promyelocytic leukemia: prima
 A:Reference number: I54081; MUID:93222087; PMID:7682097
 A:Accession: I54081

A:Status: translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-11 <DON>
 A:Cross-references: GB:S57794; NID:9299073; PIDN:AAD13888.1; PID:g4261588
 A:Note: the translation is from an incorrect reading frame
 C:Genetics:
 A:Gene: GDB:RARA
 A:Cross-references: GDB:120337; OMIM:180240
 A:Map position: 17q12-17q12

Alignment Scores:
 Pred. No.: 1.19e+05 Length: 11
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.73% Indels: 0
 DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x I54081 (1-11)

QY 1461 CGGCAGCAGTGTG 1447
 DB 5 ArgAlaAlaValLeu 9.
 |||||

RESULT 15

PN0162
 malate dehydrogenase (EC 1.1.1.37) - fungus (Fusarium sporotrichioides) (fragment)
 C:Species: Fusarium sporotrichioides
 C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 11-Nov-1994
 C:Accession: PN0162
 R:Fukaya, N.; Chow, L.P.; Sugiura, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
 submitted to JIPID, May 1994
 A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporo

A:Reference number: PN0160
 A:Accession: PN0162
 A:Molecule type: protein
 A:Residues: 1-12 <FUK>
 C:Keywords: oxidoreductase

Alignment Scores:
 Pred. No.: 1.18e+05 Length: 12
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.73% Indels: 0
 DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x PN0162 (1-12)

QY 762 GTCCTGGGCAGCA 748

```
Db
139390
acetylcholine receptor (alternative exon 5b) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 21-Jul-2000
C:Accession: I39390
R:Milovilovic, M.; Mai, Y.; Herbstreith, M.; Rubboli, F.; Tarroni, P.; Clementi, F.; Ros
A:Title: Splicing of an anti-sense Alu sequence generates a coding sequence variant for
A:Reference number: I39390; MUID:94071933; PMID:8250918
A:Accession: I39390
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-12 <RES>
A:Cross-references: GB:L18973; NID:9441143; PIDN:AAA86792.1; PID:9441144
C:Keywords: alternative splicing; neurotransmitter receptor

Alignment Scores
Pred. No.: 1.18e+05 Length: 12
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.73% Indels: 0
Gaps: 2
US-09-824-647-16 (1-2095) x I39390 (1-12)

QY 1904 CAGATGGGTCCAG 1890
11111111111111111111
Db 8 GlnAsnGlyValGln 12

RESULT 17
PH1175
T-cell receptor alpha chain V region (Cw3/Cas3) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1175
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wido
J. Exp. Med. 176, 439-447, 1992
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A:Reference number: S26512; MUID:92364546; PMID:1380061
A:Accession: PH1175
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>

Alignment Scores
Pred. No.: 1.18e+05 Length: 12
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
Gaps: 2
US-09-824-647-16 (1-2095) x PH1175 (1-12)

QY 1952 CTGTCAGAGGGGT 1966
11111111111111111111
Db 3 LeuSerGluGlyGly 7

RESULT 18
A60528
insulin-like growth factor-binding protein, serum - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-May-2000
C:Accession: A60528
R:Walton, P.E.; Baxter, R.C.; Burleigh, B.D.; Ethernon, T.D.
Comp. Biochem. Physiol. B 92, 561-567, 1989
A:Title: Purification of the serum acid-stable insulin-like growth factor binding protein
A:Reference number: A60528; MUID:89209787; PMID:2468442

A:Accession: A60528
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <WAL>

Alignment Scores
Pred. No.: 1.18e+05 Length: 12
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
Gaps: 2
US-09-824-647-16 (1-2095) x A60528 (1-12)

QY 1394 GTGGCAGCTGGGCCT 1408
11111111111111111111
Db 5 ValGlyAlaGlyPro 9

RESULT 19
S65626
phosphorylase b - rabbit (fragments)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S65626
R:Luo, S.; Martin, B.L.; Senshu, T.; Graves, D.J.
Arch. Biochem. Biophys. 318, 362-369, 1995
A:Title: Enzymatic deamination of glycogen phosphorylase and a peptide of the ph
A:Reference number: S65626; MUID:95251385; PMID:7733664
A:Accession: S65626
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-3;4-12 <LUO>

Alignment Scores
Pred. No.: 1.18e+05 Length: 12
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.73% Indels: 0
Gaps: 2
US-09-824-647-16 (1-2095) x S65626 (1-12)

QY 1084 GTGGCTGCGCAGC 1070
11111111111111111111
Db 3 ValGlyLeuAlaGly 7

RESULT 20
C30503
Ig gamma-2b chain C region (F5.5.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 16-Aug-1996
C:Accession: C30503
R:Gilmore, G.L.; Bard, J.A.; Birshstein, B.K.
J. Immunol. 141, 1754-1761, 1988
A:Title: DNA rearrangements affecting both variable and constant regions of Ig H
A:Reference number: A30503; MUID:88315788; PMID:2842402
A:Accession: C30503
A:Molecule type: mRNA
A:Residues: 1-12 <GIL>
A:Experimental source: myeloma cell line
C:Keywords: immunoglobulin

Alignment Scores
Pred. No.: 1.18e+05 Length: 12
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
Gaps: 2
US-09-824-647-16 (1-2095) x C30503 (1-12)
```

QY 413 CGGACTCTCCACGT 427
|||||
Db 7 ArgThrSerProArg 11

RESULT 21

A33520

Inhibitory diffusible factor - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 30-Sep-1993

C:Accession: A33520

R:Blat, C.; Bohlen, P.; Villaudy, J.; Chatelain, G.; Golde, A.; Harel, L.

J. Biol. Chem. 264, 6021-6024, 1989

A:Title: Isolation and amino-terminal sequence of a novel cellular growth inhibitor (inf)

A:Reference number: A33520; MUID:89197888; PMID:2703477

A:Accession: A33520

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-12 <BLA>

Alignment Scores:
Pred. No.: 12
Score: 1.18e+05
Matches: 5
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatches: 0
Query Match: 0.72%
Indels: 0
Gaps: 0
DB: 2

US-09-824-647-16 (1-2095) x A33520 (1-12)

QY 1394 GTGGAGCTGGSCCT 1408

|||||

Db 5 ValGlyAlaGlyPro 9

RESULT 22

A58375

Microcin B17 - Escherichia coli (fragment)

C:Species: Escherichia coli plasmid pPY113

C:Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 07-May-1999

C:Accession: A58375

R:Yorgey, P.; Lee, J.; Koedel, J.; Vivas, E.; Warner, P.; Jebaratnam, D.; Kolter, R.

Proc. Natl. Acad. Sci. U.S.A. 91, 4519-4523, 1994

A:Title: Posttranslational modifications in microcin B17 define an additional class of

A:Reference number: A58375; MUID:94240167; PMID:8183941

A:Accession: A58375

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-12 <YOR>

Alignment Scores:
Pred. No.: 12
Score: 1.18e+05
Matches: 5
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatches: 0
Query Match: 0.73%
Indels: 0
Gaps: 0
DB: 2

US-09-824-647-16 (1-2095) x A58375 (1-12)

QY 1143 GGTATCGGAGGAGG 1129

|||||

Db 2 GlyIleGlyGlyGly 6

RESULT 23

A32734

enkephalin precursor - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 21-Jan-2000

C:Accession: A32734

R:Micanovic, R.; Ray, P.; Kruggel, W.; Lewis, R.V.

Biochem. Biophys. Res. Commun. 118, 299-303, 1984

A:Title: Purification and sequence of an opioid peptide derived from ovine proenkephalin

A:Reference number: A32734; MUID:84128045; PMID:6546517

A:Accession: A32734
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <MIC>
C:Superfamily: proenkephalin
C:Keywords: neuropeptide; opioid peptide

Alignment Scores:
Pred. No.: 13
Score: 1.16e+05
Matches: 5
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatches: 0
Query Match: 0.73%
Indels: 0
Gaps: 0
DB: 2

US-09-824-647-16 (1-2095) x A32734 (1-13)

QY 1874 GGGAGGTGTAGGG 1860

|||||

Db 2 GlyGluValLeuGly 6

RESULT 24

G22565

R-phycoerythrin gamma-B chain - red alga (Gastrocionium coulteri) (fragment)

C:Species: Gastrocionium coulteri

C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993

C:Accession: G22565

R:Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985

A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.

A:Reference number: A22565; MUID:85182601; PMID:3886644

A:Accession: G22565

A:Molecule type: protein

A:Residues: 1-13 <KLO>

Alignment Scores:

Pred. No.: 13
Score: 1.16e+05
Matches: 5
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatches: 0
Query Match: 0.73%
Indels: 0
Gaps: 0
DB: 2

US-09-824-647-16 (1-2095) x G22565 (1-13)

QY 525 GCAGAGGCACCGTG 511

|||||

Db 2 AlaGluGlyThrVal 6

RESULT 25

PS0443

potassium channel protein Slo G3 - fruit fly (Drosophila melanogaster) (fragment)

C:Species: Drosophila melanogaster

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Feb-1997

C:Accession: PS0443

R:Adelman, J.P.; Shen, K.Z.; Kavanaugh, M.P.; Warren, R.A.; Wu, Y.N.; Lagrutta, A.

Neuron 9, 209-216, 1992

A:Title: Calcium-activated potassium channels expressed from cloned complementary

A:Reference number: JH0697; MUID:92360298; PMID:1497890

A:Accession: PS0443

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-13 <ADE>

C:Comment: This potassium channel is activated by calcium.

C:Genetics:

A:Gene: FlyBase:slo

A:Cross-references: FlyBase:FBgn0003429

C:Keywords: alternative splicing; ion channel; potassium channel; transmembrane pr

Alignment Scores:

Pred. No.: 13
Score: 1.16e+05
Matches: 5
Percent Similarity: 100.00%
Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.73% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x PS0443 (1-13)

QY 1288 GTCCAGCAGCATCT 1274
Db 3 ValGlnProArgSer 7
|||||

RESULT 26

B61458
Ig kappa chain V-I region (BLA) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
C:Accession: B61458
R:Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A:Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-asso
A:Reference number: A61458; MUID:90039128; PMID:2478651
A:Accession: B61458
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <BRO>
C:Keywords: heterotetramer; immunoglobulin

Alignment Scores:
Pred. No.: 1.16e+05 Length: 13
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.73% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x B61458 (1-13)

QY 160 CCCACACACTGAC 174
Db 8 ProThrThrLeuSer 12
|||||

RESULT 27

S47388
T-cell antigen receptor VJ junction beta chain - human

C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47388
R:Lehner, P.J.

submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47388
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35710; NID:9527515; PIDN:CAA84779.1; PID:9527516
C:Keywords: T-cell receptor

Alignment Scores:
Pred. No.: 1.16e+05 Length: 13
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.73% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x S47388 (1-13)

QY 1464 AGCCGGCAGCAGTG 1450
Db 5 SerArgAlaAlaVal 9
|||||

RESULT 28

B61233

conceptus protein 4 - cat (fragment)
C:Species: Felis silvestris catus (domestic cat)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C:Accession: B61233
R:Thatcher, M.J.D.; Shille, V.M.; Fliss, M.F.; Bazer, F.W.; Sisum, W.; Randal, S.
Biol. Reprod. 44, 108-120, 1991
A:Title: Characterization of feline conceptus proteins during pregnancy.
A:Reference number: A61233; MUID:91198359; PMID:2015342
A:Accession: B61233
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <THA>

Alignment Scores:
Pred. No.: 1.16e+05 Length: 13
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.73% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x B61233 (1-13)

QY 1169 GGGGCTGCTGTCCAA 1183
Db 5 GlyAlaAlaValGln 9
|||||

RESULT 29

B61233

conceptus protein 4 - cat (fragment)

C:Species: Felis silvestris catus (domestic cat)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C:Accession: B61233
R:Thatcher, M.J.D.; Shille, V.M.; Fliss, M.F.; Bazer, F.W.; Sisum, W.; Randal, S.
Biol. Reprod. 44, 108-120, 1991
A:Title: Characterization of feline conceptus proteins during pregnancy.
A:Reference number: A61233; MUID:91198359; PMID:2015342
A:Accession: B61233
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <THA>

Alignment Scores:

Pred. No.: 1.16e+05 Length: 13
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.73% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x B61233 (1-13)

QY 756 GGGCAGCAGTGCAG 742
Db 5 GlyAlaAlaValGln 9
|||||

RESULT 30

QVHRMM

mastoparan M-- hornet (Vespa mandarinia)

N:Alternate names: mast cell degranulating peptide
C:Species: Vespa mandarinia
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 08-Dec-1995
C:Accession: A01777
R:Hirai, Y.; Yasuhara, T.; Yoshida, R.; Nakajima, T.
Biomed. Res. 2, 447-449, 1981
A:Title: A new mast cell degranulating peptide, mastoparan-M, in the venom of the
A:Reference number: A01777
A:Accession: A01777
A:Molecule type: protein
A:Residues: 1-14 <HIR>
C:Comment: This cytoactive peptide from hornet venom induces mast cell degranulat
C:Superfamily: mastoparan
C:Keywords: amidated carboxyl end; venom

F;14/Modified site: amidated carboxyl end (Leu) #status experimental

Alignment Scores:
Pred. No.: 1.15e+05 Length: 14
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x QMWHM (1-14)

QY 571 CTGGCAAGAGCTC 585

DB 9 LeuAlaLysLeu 13

RESULT 31

B60683
malate dehydrogenase (decarboxylating) (EC 1.1.1.39) - millet (fragment)
C:Species: Panicum sp. (millet)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 24-Feb-1994
C:Accession: B60683
R:Murata, T.; Ikeda, J.; Takano, M.; Ohsugi, R.
A:Title: Comparative studies of NAD-malic enzyme from leaves of various C-4 plants.
A:Reference number: A60683
A:Accession: B60683
A:Molecule type: protein
A:Residues: 1-14 <MUR>
C:Keywords: oxidoreductase; photosynthesis

Alignment Scores:
Pred. No.: 1.15e+05 Length: 14
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x B60683 (1-14)

QY 1026 GCCCACCAGGTGCC 1040

DB 4 AlaProGlyAla 8

RESULT 32

S23376
collagen alpha chain - polychaete (Alvinella pompejana) (fragment)
C:Species: Alvinella pompejana
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-May-1998
C:Accession: S23376
R:Galli, F.; Wiedemann, H.; Mann, K.; Kuehn, K.; Timpl, R.; Engel, J.
J. Mol. Biol. 221, 209-223, 1991
A:Title: Molecular characterization of cuticle and interstitial collagens from worms col
A:Reference number: S17581; MUID:92015209; PMID:1920405
A:Accession: S23376
A:Molecule type: protein
A:Residues: 1-14 <GAI>

Alignment Scores:
Pred. No.: 1.15e+05 Length: 14
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x S23376 (1-14)

QY 1731 GCGCAGGAGGCC 1745

DB 3 AlaGInGlyPro 7

RESULT 33

PH1763

T cell receptor alpha chain V region (clone IV alpha 23-2) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1763
R:Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral b.
A:Reference number: PH1754; MUID:93301585; PMID:8391057
A:Accession: PH1763
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-14 <POR>

Alignment Scores:
Pred. No.: 1.15e+05 Length: 14
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x PH1763 (1-14)

QY 947 CTGCTGCTGTGAGG 961

DB 1 LeuCysAlaValArg 5

RESULT 34

PH1767

T cell receptor alpha chain V region (clone 2V alpha 7.2-2) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1767
R:Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral b
A:Reference number: PH1754; MUID:93301585; PMID:8391057
A:Accession: PH1767
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-14 <POR>

Alignment Scores:
Pred. No.: 1.15e+05 Length: 14
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x PH1767 (1-14)

QY 947 CTGCTGCTGTGAGG 961

DB 1 LeuCysAlaValArg 5

RESULT 35

S57574

T cell receptor V-J junctional alpha chain region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C:Accession: S57574
R:Burrows, S.R.; Sillins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argast, V.P.
submitted to the EMBL Data Library, June 1995
A:Description: T cell receptor repertoire for a viral epitope in humans is diversif
A:Reference number: S57494
A:Accession: S57574
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-14 <BUR>
A:Cross-references: EMBL:Z49959; NID:9887504; PIDN:CAA90230.1; PID:9887505
C:Keywords: T-cell receptor

Alignment Scores:
Pred. No.: 1.15e+05 Length: 14
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.73% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x S57574 (1-14)

QY 1222 AGCAGTGTCTGGT 1208

DB 4 SerSerAlaGlyGly 8

RESULT 36

JH0516

Insulin-like growth factor-binding protein 3 - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Mar-1995

C:Accession: JH0516

R:Coleman, M.E.; Pan, Y.C.E.; Ehterton, T.D.

Biochem. Biophys. Res. Commun. 181, 1131-1136, 1991

A:Title: Identification and NH2-terminal amino acid sequence of three insulin-like growth

A:Reference number: JH0515; MUID:92109718; PMID:1722398

A:Accession: JH0516

A:Molecule type: protein

A:Residues: 1-14 <COL>

A:Experimental source: serum

Alignment Scores:

Pred. No.: 1.15e+05 Length: 14
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x JH0516 (1-14)

QY 1163 GGGAGTGGGCTGT 1177

DB 1 GlySerGlyAlaAla 5

RESULT 37

JH0516

Insulin-like growth factor-binding protein 3 - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Mar-1995

C:Accession: JH0516

R:Coleman, M.E.; Pan, Y.C.E.; Ehterton, T.D.

Biochem. Biophys. Res. Commun. 181, 1131-1136, 1991

A:Title: Identification and NH2-terminal amino acid sequence of three insulin-like growth

A:Reference number: JH0515; MUID:92109718; PMID:1722398

A:Accession: JH0516

A:Molecule type: protein

A:Residues: 1-14 <COL>

A:Experimental source: serum

Alignment Scores:

Pred. No.: 1.15e+05 Length: 14
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.73% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x JH0516 (1-14)

QY 267 GGGCAGCAACTGGA 253

DB 3 GlyAlaAlaThrGly 7

RESULT 38

PH1639

Ig H chain V-D-J region (clone B-less 230) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C:Accession: PH1639

R:Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-le

A:Reference number: PH1580; MUID:93301609; PMID:8315387

A:Accession: PH1639

A:Molecule type: DNA

A:Residues: 1-14 <LEV>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Alignment Scores:

Pred. No.: 1.15e+05 Length: 14
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x PH1639 (1-14)

QY 1705 TGGCAGCAGGGGT 1719

DB 1 CysAlaArgGly 5

RESULT 39

PH1597

Ig H chain V-D-J region (wild-type clone 304) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C:Accession: PH1597

R:Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-le

A:Reference number: PH1580; MUID:93301609; PMID:8315387

A:Accession: PH1597

A:Molecule type: DNA

A:Residues: 1-14 <LEV>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Alignment Scores:

Pred. No.: 1.15e+05 Length: 14
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x PH1597 (1-14)

QY 1705 TGGCAGCAGGGGT 1719

DB 1 CysAlaArgGly 5

RESULT 40

D35141

T-cell receptor delta chain V region (105.211) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 30-May-1997

C:Accession: D35141

R:Sim, G.K.; Augustin, A.

Cell 61, 397-405, 1990

A:Title: Dominantly inherited expression of BID, an invariant undiversified T cell

A:Reference number: A35141; MUID:90242386; PMID:2110506

A:Accession: D35141
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-14 <SIM>
C:Keywords: T-cell receptor

Alignment Scores:
Pred. No.: 1.15e+05 Length: 14
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.73% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x D35141 (1-14)

QY 412 GCGATTCGAAGTAC 398

Db 8 GlytyleArgThrAsp 12

RESULT 41

leu leader peptide - Thermus aquaticus

C:Species: Thermus aquaticus

C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999

C:Accession: S00901

R:Croft, J.E.; Love, D.R.; Bergquist, P.L.

Mol. Gen. Genet. 210, 490-497, 1987

A:Title: Expression of leucine genes from an extremely thermophilic bacterium in Escheri

A:Reference number: S00901; MUID:88121725; PMID:3323845

A:Accession: S00901

A:Molecule type: DNA

A:Residues: 1-15 <CRO>

A:Cross-references: EMBL:X06604; NID:g48244; PIDN:CAA29823.1; PID:g48245

A:Note: the source is designated as Thermus thermophilus

C:Superfamily: Thermus aquaticus leu leader peptide

Alignment Scores:
Pred. No.: 1.14e+05 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x LFTWL (1-15)

QY 1625 GACAGGCTGGCCT 1639

Db 10 AspArgAlaGlyPro 14

RESULT 42

gene c-Ki-ras protein - hamster (fragment)

C:Species: Crictinae gen. sp. (hamster)

C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 28-May-1999

C:Accession: I52734

R:Takahashi, T.; Moyer, M.P.; Cano, M.; Wang, Q.J.; Mountjoy, C.P.; Sanger, W.; Adrian,

Carcinogenesis 16, 931-939, 1995

A:Title: Differences in molecular biological, biological and growth characteristics betw

A:Reference number: I52734; MUID:95246257; PMID:7728976

A:Accession: I52734

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-15 <RES>

A:Cross-references: GB:S77068; NID:g914176

C:Genetics:

A:Gene: c-Ki-ras

C:Superfamily: ras transforming protein; translation elongation factor Tu homology

C:Keywords: GTP binding

Alignment Scores:
Pred. No.: 1.14e+05 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 2 Gaps: 0

Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.73% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x I52734 (1-15)

QY 729 GCAGTGGCGTTGGG 715

Db 11 AlaGlyGlyValGly 15

RESULT 43

I49407

placental calcium-binding protein - western wild mouse (fragment)

C:Species: Mus spretus (western wild mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999

C:Accession: I49407

R:KO, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maesaki, Y.; Nadeau

Mamm. Genome 5, 349-355, 1994

A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.

A:Reference number: I48934; MUID:94319082; PMID:8043949

A:Accession: I49407

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-15 <RES>

A:Cross-references: EMBL:U05696; NID:g497016; PIDN:AAA61936.1; PID:g497017

C:Superfamily: S-100 protein; calmodulin repeat homology

C:Keywords: calcium binding; EF hand

Alignment Scores:
Pred. No.: 1.14e+05 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.73% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x I49407 (1-15)

QY 1322 GATAGGACCGCGG 1308

Db 9 AspLysGluProArg 13

RESULT 44

P00545

capsid protein VP19C - human herpesvirus 1 (fragment)

C:Species: human herpesvirus 1

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C:Accession: P00545

R:Davidson, M.D.; Rixon, F.J.; Davison, A.J.

J. Gen. Virol. 73, 2709-2713, 1992

A:Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of he

A:Reference number: P00544; MUID:93019027; PMID:1328483

A:Accession: P00545

A:Molecule type: protein

A:Residues: 1-15 <DAV>

A:Experimental source: strain 17

C:Genetics:

A:Gene: UL38

C:Keywords: capsid protein

Alignment Scores:
Pred. No.: 1.14e+05 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x P00545 (1-15)

QY 215 CTGCGGGCCACTTCCT 229

```
Db          |||||
            6 LeuProAlaThrPro 10

RESULT 45
B35389
urease (EC 3.5.1.5) 15K chain - Morganella morganii (fragment)
C:Species: Morganella morganii
C>Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 23-Jun-1993
C:Accession: B35389
R:Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.
J. Bacteriol. 172, 3073-3080, 1990
A:Title: Morganella morganii urease: purification, characterization, and isolation of ge
A:Reference number: A35389; MUID:90264298; PMID:2345135
A:Accession: B35389
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <HUA>
C:Keywords: hydrolase

Alignment Scores:
Pred. No.:      1.14e+05      Length:      15
Score:          5.00          Matches:      5
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      0.72%          Indels:      0
DB:              2              Gaps:      0

US-09-824-647-16 (1-2095) x B35389 (1-15)

QY      1827 ACCCCACTCGAGGG 1841
Db          |||||
            7 ThrProLeuGlyGly 11
```

Search completed: July 7, 2003, 16:12:15
Job time : 80.5 secs

SQ SEQUENCE 8 AA; 949 MW; 92341771A9D5A1B6 CRC64;

Alignment Scores:
Pred. No.: 1.04e+07 Length: 8
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.73% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x LPK_LEUMA (1-8)

QY 1568 ACGTCCTTCACACC 1554
|||||
Db 2 ThrSerPheThrPro 6

RESULT 2
THYF_PIG STANDARD; PRT; 9 AA.
AC P01255;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Thymic factor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.

RX MEDLINE=78026571; PubMed=914862;
RA Pleau J.-M., Dardenne M., Blouquit Y., Bach J.-F.;
RT "Structural study of circulating thymic factor: a peptide isolated
from pig serum. II. Amino acid sequence.";
RL J. Biol. Chem. 252:8045-8047(1977).
CC -1- MISCELLANEOUS: THE BIOLOGICAL SOURCE(S) AND PHYSIOLOGICAL
ACTIVITIES OF THIS PEPTIDE HAVE NOT BEEN DETERMINED.
DR PIR; A01523; YFPG.
FT MOD_RES 1
SQ SEQUENCE 9 AA; 876 MW; D500B8786C5B33D CRC64;

Alignment Scores:
Pred. No.: 9.22e+06 Length: 9
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x THYF_PIG (1-9)

QY 1387 AGCAGGCTGGGAGC 1401
|||||
Db 4 SerGlnGlyGlySer 8

RESULT 3
XYLA_STRSQ STANDARD; PRT; 9 AA.
AC P19149;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE xylose isomerase (EC 5.3.1.5) (Fragment).
GN XYLA.
OS Streptomyces sp. (strain NCL 82-5-1).
OC Bacteria; Actinobacteria; Actinobacteriia (class); Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1931;
RN [1]
RP SEQUENCE.
RQ MEDLINE=88326335; PubMed=3415697;
RA Pawar H.S., Kannan K., Srinivasan M.C., Vartak H.G.;
RT "Purification and characterisation of glucose (xylose) isomerase from

RT Chainia sp. (NCL 82-5-1).";
RL Biochem. Biophys. Res. Commun. 155:411-417(1988).
CC -1- FUNCTION: INVOLVED IN D-XYLOSE CATABOLISM.
CC -1- CATALYTIC ACTIVITY: D-xylose -D-xylosulose.
CC -1- COFACTOR: Magnesium; binds 2 ions per subunit (Potential).
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE XYLOSE ISOMERASE FAMILY.
DR PIR; A31576; A31576.
DR InterPro; IPR001998; xylose_isom.
DR PROSITE; PS00172; XYLOSE_ISOMERASE_1; PARTIAL.
DR PROSITE; PS00173; XYLOSE_ISOMERASE_2; PARTIAL.
KW Isomerase; Pentose shunt; Xylose metabolism; Magnesium.
FT NON_TER 9
SQ SEQUENCE 9 AA; 983 MW; F64BALED5B87DD1 CRC64;

Alignment Scores:
Pred. No.: 9.22e+06 Length: 9
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.73% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x XYLA_STRSQ (1-9)

QY 1380 GCAGGTCCGCCAC 1366
|||||
Db 3 AlaglySerAlaHis 7

RESULT 4
CEPL_ACHFU STANDARD; PRT; 11 AA.
AC P22790;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Cardio-excitatory peptide-1 (ACEP-1).
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Achatinacea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.

RX STRAIN=Perussac; TISSUE=Heart atrium;
RC MEDLINE=90211261; PubMed=2322251;
RX Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;
RT "A novel cardio-excitatory peptide isolated from the atria of the
African giant snail, Achatina fulica.";
RL Biochem. Biophys. Res. Commun. 167:777-783(1990).
CC -1- FUNCTION: POTENTIATES THE BEAT OF THE VENTRICLE, AND HAS ALSO
EXCITATORY ACTIONS ON THE PENIS RETRACTOR MUSCLE, THE BUCCAL
MUSCLE AND THE IDENTIFIED NEURONS CONTROLLING THE BUCCAL MUSCLE
MOVEMENT OF ACHATINA.
CC -1- SIMILARITY: TO POSSIBLE PEPTIDE I5 FROM APLYSIA.
DR PIR; A34662; A34662.
KW Hormone; Amidation.
FT MOD_RES 11
SQ SEQUENCE 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;

Alignment Scores:
Pred. No.: 5.88e+04 Length: 11
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.73% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x CEPL_ACHFU (1-11)

QY 100 AGCCACACGGCAGA 86
|||||
Db 6 ArgProGlnGlyArg 10

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RESULT 5
CD14_LITXA
ID CD14_LITXA STANDARD; PRT; 12 AA.
AC P56246;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Caeridin 1.4.
OS Litoria xanthomera (Orange-thighed frog), and
OS Litoria chloris (Blue-thighed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=79697, 86064;
[1]
RN SEQUENCE, AND MASS SPECTROMETRY.
RC SPECIES=L.xanthomera;
RX MEDLINE=97374000; PubMed=9230483;
RA Steinborner S.T., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.,
RA Ramsay S.L.;
RT Australian tree frog Litoria xanthomera.;
RT Australian tree frog Litoria xanthomera.;
RL J. Pept. Sci. 3:181-185(1997).
[2]
RN SEQUENCE.
RC SPECIES=L.chloris; TISSUE=Skin;
RX MEDLINE=98175802; PubMed=9516047;
RA Steinborner S.T., Currie G.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "New antibiotic caerin 1 peptides from the skin secretion of the
RT Australian tree frog Litoria chloris. Comparison of the activities of
RT the caerin 1 peptides from the genus Litoria.";
RL J. Pept. Res. 51:121-126(1998).
CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC ANTIBIOTIC ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MW=1096; METHOD=FAB.
KW Amphibian skin; Amidation.
FT MOD_RES 12 12
SQ SEQUENCE 12 AA; 1097 MW; 28225503E3772728 CRC64;

Alignment Scores:
Pred. No.: 5.8e+04 Length: 12
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x CD14_LITXA (1-12)
QY 915 GGGGGCTGGGCTG 929
DB 8 GlyGlyLeuGlyLeu 12

RESULT 6
H2AX_ONCMY
ID H2AX_ONCMY STANDARD; PRT; 12 AA.
AC P83327;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Histone H2A (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
[1]
RN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Skin mucus;
RA Fernandes J.M.O., Kemp G.D., Molle G., Smith V.J.;
RT "Antimicrobial properties of a histone H2A-like protein from skin

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RT secretions of rainbow trout, Oncorhynchus mykiss.";
RL Submitted (APR-2002) to the SWISS-PROT data bank.
CC -1- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria and antifungal activity against S.cerevisiae.
CC -1- SUBUNIT: The nucleosome is an octamer containing two molecules of
CC H2A, H2B, H3, and H4; which wrap approximately 146 bp of DNA.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- MASS SPECTROMETRY: MW=13639; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO THE HISTONE H2A FAMILY.
DR InterPro: IPR002119; Histone H2A.
DR PROSITE: PS00046; HISTONE_H2A; PARTIAL.
KW Chromosomal protein; Nucleosome core; Nuclear protein;
KW DNA-binding; Antibiotic; Fungicide; Acetylation.
FT NON_TER 1 1
FT MOD_RES 12 12 ACETYLATION.
SQ SEQUENCE 12 AA; 1202 MW; 3EF28D9668D87DD8 CRC64;

Alignment Scores:
Pred. No.: 5.8e+04 Length: 12
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x H2AX_ONCMY (1-12)
QY 1391 AGGTGGGAGCTGGG 1405
DB 3 ArgValGlyAlaGly 7

RESULT 7
RFL_CONSP
ID RFL_CONSP STANDARD; PRT; 12 AA.
AC P58805;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Conorfamide-Srl.
OS Conus spurius (Alphabet cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=192919;
[1]
RN SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=21605839; PubMed=11738233;
RA Maillo M., Aguilar M.B., Lopez-Vera E., Craig A.G., Bulaj G.,
RA Olivera B.M., Heimer de la Cotera E.P.;
RT "Conorfamide, a Conus venom peptide belonging to the Rfamidae family of
RT neuropeptides.";
RL Toxicon 40:401-407(2002).
CC -1- FUNCTION: Causes hyperactivity in mice.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=1454.8; METHOD=Electrospray.
CC -1- SIMILARITY: BELONGS TO THE FARP (FAMFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neurotoxin; Toxin; Amidation.
FT MOD_RES 12 12
SQ SEQUENCE 12 AA; 1456 MW; 2510671E49D772D3 CRC64;

Alignment Scores:
Pred. No.: 5.8e+04 Length: 12
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.73% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x RFL_CONSP (1-12)

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RC TISSUE-Parotoid gland;
 RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. Structures of the caeridins from
 RL Litoria caerulea."
 RL J. Chem. Soc. Perkin Trans. 1:573-576(1993).
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
 CC ANTI-BIOTIC ACTIVITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
 CC GLANDS.
 CC -1- MASS SPECTROMETRY: MW-1355; METHOD-FAB.
 CC Amphibian skin; Amidation.
 KW MOD.RES 15 15
 FT MOD.RES 15 15
 SQ SEQUENCE 15 AA; 1357 MW; 9FFIA646BD550CAE CRC64;

Alignment Scores:
 Pred. No.: 5.57e+04 Length: 15
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.72% Indels: 0
 DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x CDN5_LITCE (1-15)

QY 915 GGGGGCTGGGGCTG 929
 Db 11 GlyGlyLeuGlyLeu 15

RESULT 12

CX1B_CONBE
 ID CX1B_CONBE STANDARD; PRT; 15 AA.
 AC PS8624;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Conotoxin BeTXib.
 OS Conus betulinus (Beech cone).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 CC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=89764;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.

TISSUE-Venom;
 RX MEDLINE-20058566; PubMed-10591037;
 RA Chen J.-S., Fan C.-X., Hu K.-P., Wei K.-H., Zhong M.-N.;
 RT "Studies on conotoxins of Conus betulinus."
 RL J. Nat. Toxins 8:341-349(1999).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- MASS SPECTROMETRY: MW-1642.5; METHOD-MALDI.
 CC -1- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS.
 KW Neurotoxin; Toxin.
 FT DISULFID 1 9 PROBABLE.
 FT DISULFID 2 12 PROBABLE.
 FT DISULFID 6 13 PROBABLE.
 SQ SEQUENCE 15 AA; 1650 MW; 3749B4F08E311337 CRC64;

Alignment Scores:
 Pred. No.: 5.57e+04 Length: 15
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.72% Indels: 0
 DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x CX1B_CONBE (1-15)

QY 673 TCGTGTGAGCTGCC 687
 Db 1 CysCysGluLeuPro 5

RESULT 13

DIDH_PSESP

ID DIDH_PSESP STANDARD; PRT; 15 AA.
 AC P80701;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE 3-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.50) (3-alpha-HSD)
 DE (hydroxyprostaglandin dehydrogenase) (HSD29) (Fragment).
 OS Pseudomonas sp.
 CC Bacteria; Proteobacteria.
 OX NCBI_TaxID=306;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-97100200; PubMed-8944761;
 RA Oppermann U.C.T., Maser E.;
 RT "Characterization of a 3 alpha-hydroxysteroid dehydrogenase/carbonyl
 RL reductase from the Gram-negative bacterium Comamonas testosteroni."
 RL Eur. J. Biochem. 241:744-749(1996).
 CC -1- FUNCTION: ALONG WITH THE 3 ALPHA-HYDROXYSTEROID DEHYDROGENASE AND
 CC A/B RING STEROIDS, IT ALSO REDUCES SEVERAL XENOBIOTIC CARBONYL
 CC COMPOUNDS, INCLUDING A METYRAPON-BASED CLASS OF INSECTICIDES, TO
 CC THE RESPECTIVE ALCOHOL METABOLITES.
 CC -1- CATALYTIC ACTIVITY: Androstene + NAD(P)(+) = 5-alpha-androstane-
 CC 3,17-dione + NAD(P)H.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 DR InterPro: IPR002198; ADH_short.
 DR PROSITE: PS00061: ADH_SHORT; PARTIAL.
 KW Oxidoreductase; NAD.
 FT DOMAIN 6 >15 INVOLVED IN COFACTOR BINDING
 FT NON_TER 15 15 (BY SIMILARITY).
 FT SEQUENCE 15 AA; 1315 MW; 9506860D070A7790 CRC64;
 SQ SEQUENCE 15 AA; 1315 MW; 9506860D070A7790 CRC64;
 Alignment Scores:
 Pred. No.: 5.57e+04 Length: 15
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.73% Indels: 0
 DB: 1 Gaps: 0
 US-09-824-647-16 (1-2095) x DIDH_PSESP (1-15)
 QY 1193 GCCTCTGGGATTGA 1179
 Db 9 AlaserglyleGly 13
 RESULT 14
 LPL_THETH
 ID LPL_THETH STANDARD; PRT; 15 AA.
 AC P21234;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Leu leader peptide.
 OS Thermus thermophilus.
 CC Bacteria; Thermus/Deinococcus group; Deinococci; Thermales;
 CC Thermaceae; Thermus.
 OX NCBI_TaxID=274;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-HB8 / ATCC-27634;
 RA Croft J.E., Love D.R., Bergquist P.L.;
 RT "Expression of leucine genes from an extremely thermophilic bacterium
 RL in Escherichia coli."
 RL Mol. Gen. Genet. 210:490-497(1987).
 CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
 CC OF LEUCINE.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; X06604; CAA29823.1; -
DR PIR; S00901; LFTWL.
KW Leader peptide; Leucine biosynthesis.
SQ SEQUENCE 15 AA; 1666 MW; C2F107A386D7620B CRC64;

Alignment Scores:
Pred. No.: 5.57e+04 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x LPL_THETH (1-15)

OY 1625 GACAGGCTGGGCCT 1639
DB 10 AspArgAlaGlyPro 14
|||||

RESULT 15
PGKH_PHYPA STANDARD; PRT; 15 AA.
AC P80659;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phosphoglycerate kinase, chloroplast (EC 2.7.2.3) (Fragment).
OS Physcomitrella patens (Moss).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Funariaceae; Funariales; Funariaceae; Physcomitrella.
OX NCBI_TaxID=32118;
RN [1]
RP SEQUENCE.
RC TISSUE=Protonema;
RX MEDLINE=97275459; PubMed=9129336;
RA Kasten B., Buck F., Nuske J., Reski R.;
RT "Cytokinin affects nuclear- and plastome-encoded energy-converting
RT plastid enzymes.";
RL Planta 201:261-272(1997).
CC -1- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate -> ADP + 3-
CC phospho-D-glyceroyl phosphate.
CC -1- PATHWAY: Calvin cycle.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.
DR InterPro: IPR001576; PGK.
DR PROSITE: PS00111; GLYCERATE KINASE; PARTIAL.
KW Transferase; Kinase; 15
FT NON_TER 15
SQ SEQUENCE 15 AA; 1531 MW; 56A5ECC1F677EEC6 CRC64;

Alignment Scores:
Pred. No.: 5.57e+04 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x PGKH_PHYPA (1-15)

OY 168 ACTGAGCAGGCATCT 182
DB 3 ThrGlutAlaSer 7
|||||

RESULT 16
PGKH_PHYPA STANDARD; PRT; 15 AA.
AC P80659;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phosphoglycerate kinase, chloroplast (EC 2.7.2.3) (Fragment).
OS Physcomitrella patens (Moss).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Funariaceae; Funariales; Funariaceae; Physcomitrella.
OX NCBI_TaxID=32118;
RN [1]
RP SEQUENCE.
RC TISSUE=Protonema;
RX MEDLINE=97275459; PubMed=9129336;
RA Kasten B., Buck F., Nuske J., Reski R.;
RT "Cytokinin affects nuclear- and plastome-encoded energy-converting
RT plastid enzymes.";
RL Planta 201:261-272(1997).
CC -1- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate -> ADP + 3-
CC phospho-D-glyceroyl phosphate.
CC -1- PATHWAY: Calvin cycle.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.
DR InterPro: IPR001576; PGK.
DR PROSITE: PS00111; GLYCERATE KINASE; PARTIAL.
KW Transferase; Kinase; 15
FT NON_TER 15
SQ SEQUENCE 15 AA; 1531 MW; 56A5ECC1F677EEC6 CRC64;

Alignment Scores:
Pred. No.: 5.57e+04 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x PGKH_PHYPA (1-15)

OY 168 ACTGAGCAGGCATCT 182
DB 3 ThrGlutAlaSer 7
|||||

RESULT 16
PGKH_PHYPA STANDARD; PRT; 15 AA.
AC P80659;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phosphoglycerate kinase, chloroplast (EC 2.7.2.3) (Fragment).
OS Physcomitrella patens (Moss).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Funariaceae; Funariales; Funariaceae; Physcomitrella.
OX NCBI_TaxID=32118;
RN [1]
RP SEQUENCE.
RC TISSUE=Protonema;
RX MEDLINE=97275459; PubMed=9129336;
RA Kasten B., Buck F., Nuske J., Reski R.;
RT "Cytokinin affects nuclear- and plastome-encoded energy-converting
RT plastid enzymes.";
RL Planta 201:261-272(1997).
CC -1- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate -> ADP + 3-
CC phospho-D-glyceroyl phosphate.
CC -1- PATHWAY: Calvin cycle.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.
DR InterPro: IPR001576; PGK.
DR PROSITE: PS00111; GLYCERATE KINASE; PARTIAL.
KW Transferase; Kinase; 15
FT NON_TER 15
SQ SEQUENCE 15 AA; 1531 MW; 56A5ECC1F677EEC6 CRC64;

UC25_MAIZE
ID UC25_MAIZE STANDARD; PRT; 15 AA.
AC P80631;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 77)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC Clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.9, ITS MW IS: 31.6 kDa.
DR Maize-2DPAGE; P80631; COLEOPTILE.
DR MaizedB; 123957; -
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1580 MW; 83C54CF0CE1614D0 CRC64;

Alignment Scores:
Pred. No.: 5.57e+04 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.73% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x UC25_MAIZE (1-15)

OY 1861 GGAGCGCTCAGCAGA 1847
DB 3 GlyGlyLeuSerArg 7
|||||

RESULT 17
URE2_MORMO STANDARD; PRT; 15 AA.
AC P17338;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Urease beta subunit (EC 3.5.1.5) (15 kDa subunit) (Urea
DE amidohydrolase) (Fragment).
GN UREB.
OS Morganella morganii (Proteus morganii).
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Morganella.
OX NCBI_TaxID=582;
RN [1]
RP SEQUENCE.
RC MEDLINE=90264298; PubMed=2345135;
RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
RT "Morganella morganii urease: purification, characterization, and
RT isolation of gene sequences.";
RL J. Bacteriol. 172:3073-3080(1990).
CC -1- CATALYTIC ACTIVITY: Urea + H(2)O -> CO(2) + 2 NH(3).
CC -1- SUBUNIT: (ALPHA, BETA, GAMMA)(3) (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHER UREASES BETA SUBUNITS.
DR PIR; B35389; B35389.
KW Hydrolase.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1530 MW; 2D98944F2F20C7E8 CRC64;

Alignment Scores:
Pred. No.: 5.57e+04 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.73% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x UC25_MAIZE (1-15)

OY 1861 GGAGCGCTCAGCAGA 1847
DB 3 GlyGlyLeuSerArg 7
|||||

RESULT 17
URE2_MORMO STANDARD; PRT; 15 AA.
AC P17338;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Urease beta subunit (EC 3.5.1.5) (15 kDa subunit) (Urea
DE amidohydrolase) (Fragment).
GN UREB.
OS Morganella morganii (Proteus morganii).
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Morganella.
OX NCBI_TaxID=582;
RN [1]
RP SEQUENCE.
RC MEDLINE=90264298; PubMed=2345135;
RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
RT "Morganella morganii urease: purification, characterization, and
RT isolation of gene sequences.";
RL J. Bacteriol. 172:3073-3080(1990).
CC -1- CATALYTIC ACTIVITY: Urea + H(2)O -> CO(2) + 2 NH(3).
CC -1- SUBUNIT: (ALPHA, BETA, GAMMA)(3) (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHER UREASES BETA SUBUNITS.
DR PIR; B35389; B35389.
KW Hydrolase.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1530 MW; 2D98944F2F20C7E8 CRC64;

Alignment Scores:
Pred. No.: 5.57e+04 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.73% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x UC25_MAIZE (1-15)

OY 1861 GGAGCGCTCAGCAGA 1847
DB 3 GlyGlyLeuSerArg 7
|||||

RESULT 17
URE2_MORMO STANDARD; PRT; 15 AA.
AC P17338;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Urease beta subunit (EC 3.5.1.5) (15 kDa subunit) (Urea
DE amidohydrolase) (Fragment).
GN UREB.
OS Morganella morganii (Proteus morganii).
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Morganella.
OX NCBI_TaxID=582;
RN [1]
RP SEQUENCE.
RC MEDLINE=90264298; PubMed=2345135;
RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
RT "Morganella morganii urease: purification, characterization, and
RT isolation of gene sequences.";
RL J. Bacteriol. 172:3073-3080(1990).
CC -1- CATALYTIC ACTIVITY: Urea + H(2)O -> CO(2) + 2 NH(3).
CC -1- SUBUNIT: (ALPHA, BETA, GAMMA)(3) (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHER UREASES BETA SUBUNITS.
DR PIR; B35389; B35389.
KW Hydrolase.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1530 MW; 2D98944F2F20C7E8 CRC64;

Alignment Scores:
Pred. No.: 5.57e+04 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.73% Indels: 0
DB: 1 Gaps: 0

Pred. No.: 5.57e+04 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x URE2_MORMO (1-15)

Qy 1827 ACCCACTCGGAGG 1841

Db 7 ThrProLeuGlyGly 11

RESULT 18

COW2_CONPU

ID COW2_CONPU STANDARD; PRT; 8 AA.

AC P58785;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Leu-contrypphan-P.

OS Conus purpurascens (Purple cone).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;

OC Neogastropoda; Conoidea; Conidae; Conus.

OX NCBI_TaxID=41690;

RN [1]

RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.

RC STRAIN=Clipperton Island; TISSUE=Venom;

RX MEDLINE=9538839; PubMed=10461743;

RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,

RA Olivera B.M.;

RT "A novel D-leucine-containing Conus peptide: diverse conformational

RT dynamics in the contrypphan family.";

RL J. Pept. Res. 54:93-99(1999).

CC -1- TISSUE SPECIFICITY: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.

CC -1- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.

CC -1- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.

KW Toxin; Hydroxylation; D-amino acid.

FT DISULFID 2

FT MOD RES 4 4 D-LEUCINE.

SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Alignment Scores:

Pred. No.: 1.04e+07 Length: 8
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.58% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x COW2_CONPU (1-8)

Qy 945 GGCTGTGCTG 956

Db 1 GlyCysValLeu 4

RESULT 19

NS3_MYCTU

ID NS3_MYCTU STANDARD; PRT; 8 AA.

AC P81152;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE 30 kDa non-secretory protein 3 (Fragment).

OS Mycobacterium tuberculosis.

OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;

OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

OX NCBI_TaxID=1773;

RN [1]

RP SEQUENCE.

RC STRAIN=H37Rv;

RA Prasad H.K., Annappurna P.S.;

RL Submitted (DEC-1997) to the SWISS-PROT data bank.
CC -1- CAUTION: We are unable to find this protein in the translation of
CC the genome of strain H37Rv.

FT NON_TER 1 1

FT NON_TER 8 8

SQ SEQUENCE 8 AA; 919 MW; 8D3DC40B19CDC2D2 CRC64;

Alignment Scores:

Pred. No.: 1.04e+07 Length: 8
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.58% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x NS3_MYCTU (1-8)

Qy 815 GTGTAGCGTTC 804

Db 1 ValValAlaPhe 4

RESULT 20

RS7_MYCIT

ID RS7_MYCIT STANDARD; PRT; 8 AA.

AC P33564;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 01-FEB-1994 (Rel. 28, Last annotation update)

DE 30S ribosomal protein S7 (Fragment).

GN RPS6.

OS Mycobacterium intracellulare.

OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;

OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

OX NCBI_TaxID=1767;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93197130; PubMed=8451173;

RA Nair J., Rouse D.A., Morris S.L.;

RT "Nucleotide sequence analysis of the ribosomal S12 gene of

RT Mycobacterium intracellulare.";

RT Nucleic Acids Res. 21:1039-1039(1993).

CC -1- FUNCTION: PROTEIN S7 BINDS SPECIFICALLY TO PART OF THE 3' END OF

CC 16S RIBOSOMAL RNA (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; L08171; AAA25376.1; -

DR PIR; S35538; S35538.

DR InterPro; IPR000235; Ribosomal_S7.

DR PROSITE; PS00052; RIBOSOMAL_S7; PARTIAL.

KW Ribosomal protein; rRNA-binding.

FT INIT_MET 0 0 BY SIMILARITY.

FT NON_TER 8 8

SQ SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;

Alignment Scores:

Pred. No.: 1.04e+07 Length: 8
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.58% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x RS7_MYCIT (1-8)

Qy 1407 GGCCACGCTCC 1396

```
DB:
|||||
4 GlyProAlaPro 7

RESULT 21
UF06_MOUSE
ID UF06_MOUSE STANDARD; PRT; 8 AA.
AC P38644;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
using preparative two-dimensional gel electrophoresis."
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.2, ITS MW IS: 50 kDa.
FT NON_TER 8
SQ SEQUENCE 8 AA; 817 MW; A35DD878676B05B1 CRC64;

Alignment Scores:
Pred. No.: 1.04e+07 Length: 8
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.58% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x UF06_MOUSE (1-8)

QY 112 CCCGGAGGAGCC 123
DB:
|||||
4 ProGlyGlyAla 7

RESULT 22
UF06_MOUSE
ID UF06_MOUSE STANDARD; PRT; 8 AA.
AC P38644;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
using preparative two-dimensional gel electrophoresis."
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.2, ITS MW IS: 50 kDa.
FT NON_TER 8
SQ SEQUENCE 8 AA; 817 MW; A35DD878676B05B1 CRC64;

Alignment Scores:
Pred. No.: 1.04e+07 Length: 8
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.58% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x UF06_MOUSE (1-8)

QY 112 CCCGGAGGAGCC 123
DB:
|||||
4 ProGlyGlyAla 7

RESULT 23
UPAA_HUMAN
ID UPAA_HUMAN STANDARD; PRT; 8 AA.
AC P30096;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing."
RL Electrophoresis 13:707-714(1992).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 7, ITS MW IS: 12 kDa.
DR SWISS-2DPAGE; P30096; HUMAN.
FT NON_TER 1
FT VARIANT 5
FT 5 F -> P.
FT 5 /FTID-VAR_000004.
FT NON_TER 8
SQ SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;

Alignment Scores:
Pred. No.: 1.04e+07 Length: 8
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.58% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x UPAA_HUMAN (1-8)

QY 936 TTTTACCCAGGC 947
DB:
|||||
5 PheTyrProGly 8

RESULT 24
VGLG_HSV2B
ID VGLG_HSV2B STANDARD; PRT; 8 AA.
AC P81780;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Glycoprotein G (Fragment).
OS Herpes simplex virus (type 2 / strain B4327UR).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=103921;
RN [1]
RP SEQUENCE.
RA Liljeqvist J.-A., Svennerholm B., Bergstrom T.;
RL Submitted (APR-1999) to the SWISS-PROT data bank.
CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
CC 2: GH, GB, GC, GD, GI, AND GE.
CC -1- MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV-2 THAN IN
CC HSV-1.
KW Glycoprotein.
```

```
DB:
|||||
1036 CCTGGTGGGCC 1025
DB:
|||||
4 ProGlyGlyAla 7

RESULT 23
UPAA_HUMAN
ID UPAA_HUMAN STANDARD; PRT; 8 AA.
AC P30096;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing."
RL Electrophoresis 13:707-714(1992).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 7, ITS MW IS: 12 kDa.
DR SWISS-2DPAGE; P30096; HUMAN.
FT NON_TER 1
FT VARIANT 5
FT 5 F -> P.
FT 5 /FTID-VAR_000004.
FT NON_TER 8
SQ SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;

Alignment Scores:
Pred. No.: 1.04e+07 Length: 8
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.58% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x UPAA_HUMAN (1-8)

QY 936 TTTTACCCAGGC 947
DB:
|||||
5 PheTyrProGly 8

RESULT 24
VGLG_HSV2B
ID VGLG_HSV2B STANDARD; PRT; 8 AA.
AC P81780;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Glycoprotein G (Fragment).
OS Herpes simplex virus (type 2 / strain B4327UR).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=103921;
RN [1]
RP SEQUENCE.
RA Liljeqvist J.-A., Svennerholm B., Bergstrom T.;
RL Submitted (APR-1999) to the SWISS-PROT data bank.
CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
CC 2: GH, GB, GC, GD, GI, AND GE.
CC -1- MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV-2 THAN IN
CC HSV-1.
KW Glycoprotein.
```


FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 683 MW; 7B47686772C86588 CRC64;
 Alignment Scores:
 Pred. No.: 1.04e+07 Length: 8
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.58% Indels: 0
 DB: 0 Gaps: 0

US-09-824-647-16 (1-2095) x VGLG_HSV2B (1-8)

QY 1834 AGTGGGTCGCC 1823

Db 2 SerGlyValPro 5
 |||||

RESULT 25

AL11_CARMA
 ID AL11_CARMA STANDARD; PRT; 9 AA.
 AC P81814;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin II.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 OC Brachyura; Eubrachyura; Portunoidae; Fortuinidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]

RP SEQUENCE.

RC TISSUE=Cerebral ganglion, and Thoracic ganglion;

RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;

RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).

CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.

KW Neuropeptide; Amidation; Multigene family.

FT MOD_RES 9 9 AMIDATION.

SQ SEQUENCE 9 AA; 927 MW; 832D79CDB46D861 CRC64;

Alignment Scores:
 Pred. No.: 9.22e+06 Length: 9
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.58% Indels: 0
 DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x AL11_CARMA (1-9)

QY 1545 GCTACGGCCAG 1534

Db 1 AlaThrGlycin 4
 |||||

RESULT 26

CONO_CONST
 ID CONO_CONST STANDARD; PRT; 9 AA.
 AC P05487;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Arg-conopressin S.
 OS Conus striatus (Striated cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6493;
 RN [1]

RP SEQUENCE.

RX MEDLINE=88058932; PubMed=3680228;
 RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
 RA Gray W.R., Olivera B.M.;
 RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
 RT peptides from Conus geographus and Conus straitus venoms.";
 RL J. Biol. Chem. 262:15821-15824(1987).
 RN [2]
 RP REVIEW.
 RX MEDLINE=89024586; PubMed=3052286;
 RA Gray W.R., Olivera B.M., Cruz L.J.;
 RT "Peptide toxins from venomous Conus snails.";
 RL Annu. Rev. Biochem. 57:665-700(1988).
 CC -1- FUNCTION: Targets vasopressin-oxytocin related receptors.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR PIR; B28495; B28495.
 DR InterPro; IPR000981; Neurhyp_horm.
 DR Pfam; PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1031 MW; 17EB176EB4540050 CRC64;

Alignment Scores:
 Pred. No.: 9.22e+06 Length: 9
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.58% Indels: 0
 DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x CONO_CONST (1-9)

QY 307 TGCCACGGGCG 318

Db 6 CysProArgGly 9
 |||||

RESULT 27

DL_NEPNO
 ID DL_NEPNO STANDARD; PRT; 9 AA.
 AC P24816;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-MAR-1992 (Rel. 21, Last annotation update)
 DE Gastrin/cholecystokinin-like peptide D1.
 OS Nephrops norvegicus (Norway lobster).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 OC Astacidea; Nephropoidea; Nephropidae; Nephrops.
 OX NCBI_TaxID=6829;
 RN [1]

RP SEQUENCE.

RC TISSUE=Stomach;

RX MEDLINE=92082847; PubMed=1747388;

RA Favrel P., Kegeles G., Sedlmeier D., Keller R., van Wormhoudt A.;
 RT "Structure and biological activity of crustacean gastrointestinal
 RT peptides identified with antibodies to gastrin/cholecystokinin.";
 RL Biochimie 73:1233-1239(1991).

CC -1- FUNCTION: MAY CONTROL DIGESTION PROCESSES IN CRUSTACEANS.

CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.

DR PIR; A48398; A48398.

KW Hormone.

SQ SEQUENCE 9 AA; 1038 MW; 60EC79CAB6D8787B CRC64;

Alignment Scores:

Pred. No.: 9.22e+06 Length: 9
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.58% Indels: 0
 DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x DL_NEPNO (1-9)
QY 1955 TCAGAGGGGT 1966
Db 1 Ser-Glucglygly 4
RESULT 28
DNFI_LOCM1 STANDARD; PRT; 9 AA.
AC P16339;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Locupressin (Diuretic neuropeptide Fl/F2).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_Taxid=7004;
RN [1]
RP SEQUENCE.
RC TISSUE-Suboesophageal ganglion, and Thoracic ganglion;
RX MEDLINE=88077077; PubMed=3689410;
RA Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,
RA Delaage M., Schooley D.A.;
RT "Identification of an arginine vasopressin-like diuretic hormone from
RT Locusta migratoria".
RL Biochem. Biophys. Res. Commun. 149:180-186(1987).
CC -1- FUNCTION: DIURETIC HORMONE.
CC -1- SUBUNIT: F2 IS AN ANTIPARALLEL DISULFIDE LINKED DIMER OF F1.
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A29477; A29477.
DR InterPro; IPR000981; Neurohyp_horm.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Neuropeptide; Amidation.
FT DISULFID 1 6 IN FL.
FT DISULFID 1 1 INTERCHAIN (WITH C-6') (IN F2).
FT DISULFID 6 6 INTERCHAIN (WITH C-1') (IN F2).
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;
Alignment Scores:
Pred. No.: 9.22e+06 Length: 9
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.58% Indels: 0
DB: 1 Gaps: 0
US-09-824-647-16 (1-2095) x DNFI_LOCM1 (1-9)
QY 307 TGCCAGGGGC 318
Db 6 CysProArggly 9
RESULT 29
FAR9_ASCSU STANDARD; PRT; 9 AA.
AC P43172;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRFamide-like neuropeptide AF9.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_Taxid=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;

*Eight novel FMRFamide-like neuropeptides isolated from the nematode
RT Ascaris suum.*
RL Peptides 16:491-500(1995).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;
Alignment Scores:
Pred. No.: 9.22e+06 Length: 9
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.58% Indels: 0
DB: 1 Gaps: 0
US-09-824-647-16 (1-2095) x FAR9_ASCSU (1-9)
QY 283 CCACGGCCTCTG 272
Db 4 ProArgProleu 7
RESULT 30
OXYA_SCYCA STANDARD; PRT; 9 AA.
ID OXYA_SCYCA
AC P42996;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Asvatocin.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_Taxid=7830;
RN [1]
RP SEQUENCE.
RC TISSUE-Pituitary; PubMed=7972045;
RX MEDLINE=95062247; Chauvet J., Chauvet M.-T., Acher R.;
RX Chauvet J., Rouille Y., Chauvet C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
RT fishes: asvatocin and phasvatocin, two oxytocin-like peptides
RT isolated from the spotted dogfish (Scyliorhinus canicula).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -1- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohyp_horm.
DR InterPro; IPR001230; Prenyl_site.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 982 MW; 17EDD76EB4440404B CRC64;
Alignment Scores:
Pred. No.: 9.22e+06 Length: 9
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.58% Indels: 0
DB: 1 Gaps: 0
US-09-824-647-16 (1-2095) x OXYA_SCYCA (1-9)
QY 683 TGCCAGTGGGA 694
Db 6 CysProValgly 9
RESULT 31
OXYF_SCYCA STANDARD; PRT; 9 AA.
ID OXYF_SCYCA

AC P42997;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Phasvatocin.
 OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphi; Galeoidea; Carchariniiformes;
 OC Scyliorhinidae; Scyliorhinus.
 OX NCBI_TaxID=7830;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Pituitary;
 RX MEDLINE=95062247; PubMed=7972045;
 RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
 RT "Special evolution of neurohypophysial hormones in cartilaginous
 fishes: asvatocin and phasvatocin, two oxytocin-like peptides
 isolated from the spotted dogfish (Scyliorhinus canicula).";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
 CC -1- FUNCTION: DISPLAYS OXYTOCIN ACTIVITY ON RAT UTERUS.
 CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR InterPro; IPR000981; Neurohyp.horm.
 DR InterPro; IPR001230; Prenyl_site.
 DR Pfam; PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD_RES 9 9
 FT SEQUENCE 9 AA; 1016 MW; 17EDD76EB4449DB CRC64;
 Alignment Scores:
 Pred. No.: 9.22e+06 Length: 9
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.58% Indels: 0
 DB: 1 Gaps: 0
 US-09-824-647-16 (1-2095) x OXYF_SCYCA (1-9)
 OY 683 TGCCAGTGGGA 694
 Db 6 CysProValGly 9
 RESULT 32
 OXYT_CYPCA
 ID OXYT_CYPCA STANDARD; PRT; 9 AA.
 AC P23879;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Vasotocin.
 OS Cyprinus carpio (Common carp), and
 OS Petromyzon marinus (Sea lamprey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 OX NCBI_TaxID=7962, 7757;
 RN [1]
 RP SEQUENCE.
 RC SPECIES-C.carpio; TISSUE-Pituitary;
 RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
 RT "Characterization of neurohypophyseal hormones from a fresh water bony
 fish, the carp (Cyprinus carpio). Comparison with hormones from sea
 water bony fishs.";
 RL Comp. Biochem. Physiol. 14:245-254(1965).
 RN [2]
 RP SEQUENCE.
 RC SPECIES-P.marinus; TISSUE-Pituitary;
 RX MEDLINE=86225976; PubMed=3371648;
 RA Lane T.F., Sower S.A., Kawachi H.;
 RT "Arginine vasotocin from the pituitary gland of the lamprey
 (Petromyzon marinus): isolation and amino acid sequence.";

RL Gen. Comp. Endocrinol. 70:152-157(1988).
 CC -1- FUNCTION: ANTIDIURETIC HORMONE.
 CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR PIR; B61364; B61364.
 DR PIR; S06375; S06375.
 DR InterPro; IPR000981; Neurohyp.horm.
 DR Pfam; PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD_RES 9 9
 FT SEQUENCE 9 AA; 1053 MW; 17EB176EB456D04B CRC64;
 Alignment Scores:
 Pred. No.: 9.22e+06 Length: 9
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.58% Indels: 0
 DB: 1 Gaps: 0
 US-09-824-647-16 (1-2095) x OXYT_CYPCA (1-9)
 OY 307 TGCCACGGGCG 318
 Db 6 CysProArgGly 9
 RESULT 33
 OXYV_SQUAC
 ID OXYV_SQUAC STANDARD; PRT; 9 AA.
 AC P43000;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Valitocin.
 OS Squalus acanthias (Spiny dogfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
 OX NCBI_TaxID=7797;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=73031727; PubMed=5083097;
 RA Acher R., Chauvet J., Chauvet M.-T.;
 RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
 isolated from a cartilaginous fish, Squalus acanthias.";
 RL Eur. J. Biochem. 29:12-19(1972).
 RN [2]
 RP SEQUENCE.
 RX MEDLINE=72128038; PubMed=4622083;
 RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
 RT "Identification of 2 new neurohypophyseal hormones, valitocin (Val8-
 oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
 spiny dog-fish (Squalus acanthias).";
 RL C. R. Acad. Sci., D. Sci. Nat. 274:313-316(1972).
 CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR InterPro; IPR000981; Neurohyp.horm.
 DR InterPro; IPR001230; Prenyl_site.
 DR Pfam; PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD_RES 9 9
 FT SEQUENCE 9 AA; 996 MW; 17EDD76EB456D04B CRC64;
 Alignment Scores:
 Pred. No.: 9.22e+06 Length: 9
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.58% Indels: 0
 DB: 1 Gaps: 0
 US-09-824-647-16 (1-2095) x OXYV_SQUAC (1-9)

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CC or send an email to license@isb-sib.ch).
-----
CC EMBL; M83692; AAA22122.1;
CC DR PIR; B41983; B41983.
CC KW Hypothetical protein.
CC FT NON_TER 9
CC SQ SEQUENCE 9 AA; 947 MW; DF98B5A1B417776D CRC64;
-----
Alignment Scores:
Pred. No.: 9.22e+06 Length: 9
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.58% Indels: 0
DB: 1 Gaps: 0
US-09-824-647-16 (1-2095) x YBFR_AZOVI (1-9)
QY 812 CCACGGACCTCC 823
DB 4 ProArgThrSer 7
-----
RESULT 36
BPP8_BOTIN
ID BPP8_BOTIN STANDARD; PRT; 10 AA.
AC P30426;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Bradykinin-potentiating peptide S5,1 (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
CC PIR; H37196; H37196.
CC KW Hypotensive agent; Venom.
CC FT MOD_RES 1
CC SQ SEQUENCE 10 AA; 1173 MW; 2FF835545761F6D8 CRC64;
-----
Alignment Scores:
Pred. No.: 5.45e+05 Length: 10
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.58% Indels: 0
DB: 1 Gaps: 0
US-09-824-647-16 (1-2095) x BPP8_BOTIN (1-10)
QY 464 GGCAGCACCCC 453
DB 3 GlyGlnHisPro 6
-----
RESULT 37
BRK_ONCMY
ID BRK_ONCMY STANDARD; PRT; 10 AA.
-----
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QY 683 TGCCAGTGGGA 694
DB 6 CysProValGly 9
-----
RESULT 34
SAP_STOVA
ID SAP_STOVA STANDARD; PRT; 9 AA.
AC P24047;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-MAR-1992 (Rel. 21, Last annotation update)
DE Sperm-activating peptide (SAP).
OS Stomopneustes variolaris (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Diadematacea; Phymosomatoida; Stomechinidae;
OC Stomopneustes.
OX NCBI_TaxID=7663;
RN [1]
RP SEQUENCE, AND DISULFIDE BOND.
RC TISSUE=Egg jelly;
RX MEDLINE=92097763; PubMed=1756858;
RX Yoshino K.-I., Takao T., Shimonishi Y., Suzuki N.;
RT "Determination of the amino acid sequence of an intramolecular
RT disulfide linkage-containing sperm-activating peptide by tandem mass
RT spectrometry.";
RL FEBS Lett. 294:179-182(1991).
CC -1- FUNCTION: CAUSE STIMULATION OF SPERM RESPIRATION AND MOBILITY
CC THROUGH INTRACELLULAR ALKALINIZATION, TRANSIENT ELEVATIONS OF
CC CAMP, CGMP AND CLACIUM LEVELS IN SPERM CELLS, AND TRANSIENT
CC ACTIVATION AND SUBSEQUENT INACTIVATION OF THE MEMBRANE FORM OF
CC GUANYLATE CYCLASE.
DR PIR; S19329; S19329.
FT DISULFID 3
SQ SEQUENCE 9 AA; 1010 MW; C469B3387B076EB9 CRC64;
-----
Alignment Scores:
Pred. No.: 9.22e+06 Length: 9
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.58% Indels: 0
DB: 1 Gaps: 0
US-09-824-647-16 (1-2095) x SAP_STOVA (1-9)
QY 154 TGTCAGAGGG 143
DB 3 CysProGluGly 6
-----
RESULT 35
YBFR_AZOVI
ID YBFR_AZOVI STANDARD; PRT; 9 AA.
AC P25825;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in BFR 3'region (Fragment).
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92196129; PubMed=1549605;
RX Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.,
RX Stiefel E.I.;
RT "Unification of the ferritin family of proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).
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QY		1416	CTGGCAGCAGGC	1405	
DB					
			1 LeuAlaAAlaGly	4	
 RESULT 39					
GONZ_2_CHEPR					
ID	GONZ_2_CHEPR	STANDARD;	PRT;	10 AA.	
AC	P80678;				
DT	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	16-OCT-2001	(Rel. 40, Last annotation update)			
DE	Gonadoliberin II	(Gonadotropin-releasing hormone II) (GNRH-II)			
DE	(luliberin;II).				
OS	Chelyosoma;productum.				
OC	Eukaryota; Metazoa;	Chordata; Urochordata; Ascidacea; Enterogona;			
OC	Phlebobranchia; Corellidae; Chelyosoma.				
NCBI_TaxID=71177;					
[1]					
RN	SEQUENCE.				
RX	MEDLINE=96413669; PubMed=8816823;				
RA	Fowell J.F.F.; Reska-Skinner S.M., Prakash M.O., Fischer W.H.,				
RA	Park M., Rivier J.E., Craig A.G., Mackie G.O., Sherwood N.M.;				
RT	"Two new forms of gonadotropin-releasing hormone in a protochordate				
RT	and the evolutionary implications."				
RL	Proc. Natl. Acad. Sci. U.S.A. 93:10461-10464(1996).				
CC	-1- FUNCTION: STIMULATES THE SECRETION OF BOTH LUTEINIZING AND				
CC	FOLLICLE-STIMULATING HORMONES.				
CC	-1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.				
CC	-1- SUBCELLULAR LOCATION: Secreted.				
CC	-1- TISSUE SPECIFICITY: GNRH NEURONS LIE WITHIN BLOOD SINUSES CLOSE TO				
CC	THE GONADOUCTS AND GONADS IN BOTH JUVENILES AND ADULTS, IMPLYING				
CC	THAT THE NEUROPEPTIDE IS RELEASED INTO THE BLOODSTREAM.				
CC	-1- MASS SPECTROMETRY: MW=1117.52; METHOD=MALDI.				
CC	-1- SIMILARITY: BELONGS TO THE GNRH FAMILY.				
DR	InterPro: IPR002012; Gnrh.				
KW	Hormone; Amidation.				
FT	MOD_RES 1 1	PYRROLIDONE CARBOXYLIC ACID.			
FT	DISULFID 6 6	INTERCHAIN.			
FT	MOD_RES 10 10	AMIDATION (BY SIMILARITY).			
SQ	SEQUENCE 10 AA; 1135 MW;	284B38DIEEB735A3 CRC64;			
 Alignment Scores:					
Pred. No.:	5.45e+05	Length:	10		
Score:	4.00	Matches:	4		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	0.58%	Indels:	0		
DB:	1	Gaps:	0		
 US-09-824-647-16 (1-2095) x GONZ_2_CHEPR (1-10)					
QY	465	CATGCCCGCAGGC	476		
DB					
	7	HisAlaProGly	10		
 RESULT 40					
GRP_RANRI					
ID	GRP_RANRI	STANDARD;	PRT;	10 AA.	
AC	P23260;				
DT	01-NOV-1991	(Rel. 20, Created)			
DT	01-NOV-1991	(Rel. 20, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Neuroedin C.				
OS	Rana ridibunda	(Laughing frog) (Marsh frog).			
OC	Eukaryota; Metazoa;	Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.				
NCBI_TaxID=8406;					
[1]					
RN	SEQUENCE.				
RP	TISSUE=Brain;				
RC	MEDLINE=91315477; PubMed=1859413;				
RA	Conlon J.M., O'Harte F., Vaudry H.;				

RT *Primary structures of the bombesin-like neuropeptides in frog brain
 RL show that bombesin is not the amphibian gastrin-releasing peptide.*;
 RL Biochem. Biophys. Res. Commun. 178:526-530(1991).

CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
 CC FAMILY.

DR PIR; PQ0177; PQ0177.

DR InterPro; IPR000874; Bombesin.

DR Pfam; PF02044; Bombesin; 1.

DR PROSITE; PS00257; BOMBESIN; 1.

KW Bombesin family; Amidation.

FT MOD_RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA; 1094 MW; F81FBAE862CDC371 CRC64;

Alignment Scores:
 Pred. No.: 5.45e+05 Length: 10
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.58% Indels: 0
 DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x GRP_RANKI (1-10)

QY 694 TCCCACTGGCA 683

Db 111111111111

2 SerHisTrpAla 5

RESULT 41

ODP2_BOVIN

ID ODP2_BOVIN STANDARD; PRT; 10 AA.

AC F11180;

DT 01-JUL-1989 (Rel. 11, Created)

DT 01-JUL-1989 (Rel. 11, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase

DE complex (EC 2.3.1.12) (E2) (Fragment).

GN DLAT.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE.

RX MEDLINE=88024154; PubMed=3117054;

RA Bradford A.P., Howell S., Aitken A., James L.A., Yeaman S.J.;

RT *Primary structure around the lipoyl-attachment site on the E2

RT component of bovine heart pyruvate dehydrogenase complex.*;

RL Biochem. J. 245:919-922(1987).

CC -1- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall

CC conversion of pyruvate to acetyl-CoA and CO(2). It contains

CC multiple copies of three enzymatic components: pyruvate

CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and

CC lipoyl dehydrogenase (E3).

CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-

CC acetyldihydrolipoamide.

CC -1- COFACTOR: THE E2 COMPONENT CONTAINS TWO COVALENTLY-BOUND LIPOYL

CC COFACTOR.

CC -1- SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL

CC SYMMETRY.

CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.

CC -1- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.

CC -1- SIMILARITY: CONTAINS 2 LIPOYL-BINDING DOMAINS.

DR InterPro; IPR003016; Lipoyl.

DR PROSITE; PS00189; LIPOYL; PARTIAL.

KW Glycolysis; Transferase; Acyltransferase; Repeat; Mitochondrion;

KW Lipoyl.

FT NON_TER 1 1

FT BINDING 5 5 LIPOYL.

FT NON_TER 10 10

SQ SEQUENCE 10 AA; 1066 MW; 889BECDIADD33AB1 CRC64;

Alignment Scores:
 Pred. No.: 5.45e+05 Length: 10
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.58% Indels: 0
 DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x ODP2_BOVIN (1-10)

QY 620 GAGAAGGCCACT 609

Db 111111111111

4 AspLysAlaThr 7

RESULT 42

PNEU_HUMAN

ID PNEU_HUMAN STANDARD; PRT; 10 AA.

AC P22103;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pneumadin (PNM).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RC TISSUE=Lung;

RX MEDLINE=91110910; PubMed=2274681;

RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;

RT *Pneumadin: a new lung peptide which triggers antidiuresis.*;

RL Regul. Pept. 30:77-87(1990).

CC -1- FUNCTION: ANTIDIURETIC PEPTIDE THAT TRIGGERS THE RELEASE OF ADH.

DR PIR; B33143; B33143.

KW Amidation.

FT MOD_RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA; 956 MW; 640378DAA723276B CRC64;

Alignment Scores:

Pred. No.: 5.45e+05 Length: 10
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.58% Indels: 0
 DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x PNEU_HUMAN (1-10)

QY 234 GATGCGAGGAGTG 223

Db 111111111111

7 AspAlaGlyVal 10

RESULT 43

PNEU_RAT

ID PNEU_RAT STANDARD; PRT; 10 AA.

AC P21996;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pneumadin (PNM).

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE, AND SYNTHESIS.

RC TISSUE=Lung;

RX MEDLINE=91110910; PubMed=2274681;

RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;

RT *Pneumadin: a new lung peptide which triggers antidiuresis.*;

RL Regul. Pept. 30:77-87(1990).

CC -1- FUNCTION: THIS ANTIDIURETIC PEPTIDE TRIGGERS THE RELEASE OF ADH.

DR PIR: A33143; A33143.
KW Amidation. 10 10 AMIDATION.
FT MOD_RES 10 AA; 1048 MW; 641D00DAA723276B CRC64;
SQ SEQUENCE 10 AA; 1048 MW; 641D00DAA723276B CRC64;

Alignment Scores:
Pred. No.: 5.45e+05 Length: 10
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.58% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x PNEU_RAT (1-10)

QY 234 GATGAGGAGTG 223
DB 7 ASPALAGLYVal 10

RESULT 44
RRPL_PHODV STANDARD; PRT; 10 AA.
AC P35946;

DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
DE (L protein) (fragment).
GN L.

OS Phocine distemper virus (PDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
OX NCBI_TaxID=11240;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=U1ster/88;

RX MEDLINE=92268877; PubMed=1588321;

RA Curran M.D., O'Loan D., Kennedy S., Rima B.K.;
RT "Molecular characterization of phocine distemper virus: gene order
and sequence of the gene encoding the attachment (B) protein.";

RL J. Gen. Virol. 73:1189-1194(1992).

CC -1- FUNCTION: PROBABLE COMPONENT OF THE ACTIVE POLYMERASE. IT MAY
CC SYNTHESIS IN MRNA SYNTHESIS, CAPPING, METHYLATION AND POLY(A)
CC GENE TRANSCRIPT, AND PROTEIN KINASE ACTIVITY.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC {RNA}(N).

CC -1- SIMILARITY: WITH L PROTEIN OF OTHER PARAMYXOVIRUSES.

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CC or send an email to license@isb-sib.ch).

DR EMBL: D10371; BAA01208.1;
KW Transferase; RNA-directed RNA polymerase.
FT NON_TER 10 10

SQ SEQUENCE 10 AA; 1105 MW; 9C2B7FD452D5A2D5 CRC64;

Alignment Scores:
Pred. No.: 5.45e+05 Length: 10
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.58% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x RRPL_PHODV (1-10)

QY 1877 AACCAAAATTC 1888

Db 7 AsnGlnIleLeu 10
RESULT 45
TEMK_RANTE STANDARD; PRT; 10 AA.
AC P56923;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Temporin K.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.;
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE
CC BACTERIA.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
KW Amphibian skin; Antibiotic; Amidation; Multigene family.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1123 MW; 390549B337272457 CRC64;

Alignment Scores:
Pred. No.: 5.45e+05 Length: 10
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.58% Indels: 0
DB: 1 Gaps: 0

US-09-824-647-16 (1-2095) x TEMK_RANTE (1-10)

QY 702 CTGCTGCCCAAT 713

Db 1 LeuLeuProAsn 4

Search completed: July 7, 2003, 16:08:30
Job time : 33.5 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: July 7, 2003, 16:07:27 ; Search time 133.5 Seconds

(without alignments)

6466.947 Million cell updates/sec

Title: US-09-824-647-16

Perfect score: 694

Sequence: 1 ccagcagcagaccatgtggac.....ataagttgtcactttctt 2095

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 671580 seqs, 206047115 residues

Word size: 1

Total number of hits satisfying chosen parameters: 6206

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Listing first 45 summaries

Command line parameters:

-O/cgn2_1/USPTO_spool/US09824647/runat_07072003_154759_26619/app_query.fasta_1.2247
-DB-SPREMBL_21 -QFMT-fastan -SUFFIX=lim.rspt -MINMATCH=0.1 -LOOPCL=0
-LOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=oligo -TRANS-human40.cdi
-LIST=45 -DOCLIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=45 -MODE=LOCAL
-OUTFMT=ptc -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=15
-USER=US09824647 -CGN_1_1_231 -runat_07072003_154759_26619 -NCPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvrius:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	6	0.9	10	2 Q8RJF1	Q8RJF1 pseudomonas

c 2	6	0.9	11	5	Q26092
c 3	5	0.7	9	11	O08979
c 4	5	0.7	9	13	P83056
c 5	5	0.7	10	6	P82923
c 6	5	0.7	10	6	Q9TRU6
c 7	5	0.7	10	8	Q9T2P3
c 8	5	0.7	10	8	Q8SHF0
c 9	5	0.7	10	8	Q8SHM2
c 10	5	0.7	10	8	Q8SHL3
c 11	5	0.7	10	8	Q8SHL0
c 12	5	0.7	10	8	Q8SHL0
c 13	5	0.7	10	8	Q8SHK1
c 14	5	0.7	10	10	Q9S905
c 15	5	0.7	10	11	O70580
c 16	5	0.7	10	12	O90346
c 17	5	0.7	11	4	O60614
c 18	5	0.7	11	4	Q9NY38
c 19	5	0.7	11	4	Q15937
c 20	5	0.7	11	10	O65901
c 21	5	0.7	12	2	O54226
c 22	5	0.7	12	4	Q9B249
c 23	5	0.7	12	4	Q13695
c 24	5	0.7	12	4	Q9UC37
c 25	5	0.7	12	10	Q93X21
c 26	5	0.7	12	10	Q93WF2
c 27	5	0.7	12	12	O69232
c 28	5	0.7	12	12	O69232
c 29	5	0.7	13	11	Q91XP1
c 30	5	0.7	13	12	Q9E1V4
c 31	5	0.7	13	12	Q9E1V3
c 32	5	0.7	13	12	Q9E1V2
c 33	5	0.7	13	12	Q9E1V0
c 34	5	0.7	13	12	Q9E1U9
c 35	5	0.7	13	12	Q9E1U8
c 36	5	0.7	13	12	Q9E1U6
c 37	5	0.7	13	12	Q9E1U5
c 38	5	0.7	13	12	Q9E1U4
c 39	5	0.7	13	12	Q9E1U3
c 40	5	0.7	13	12	Q9E1U2
c 41	5	0.7	13	12	Q9E1U1
c 42	5	0.7	13	12	Q9E1U0
c 43	5	0.7	13	12	Q9E1T9
c 44	5	0.7	13	12	Q9E1T8
c 45	5	0.7	14	2	Q52840

ALIGNMENTS

RESULT 1

ID	Q8RJF1	PRELIMINARY;	PRG;	10 AA.
AC	Q8RJF1			
DT	01-JUN-2002	(TREMBLrel. 21, Created)		
DT	01-JUN-2002	(TREMBLrel. 21, Last sequence update)		
DE	Porin-like protein (Fragment)			
OS	Pseudomonas fluorescens			
OC	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;			
OC	Pseudomonas			
OX	NCBI_TaxID=294;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NC16-2, TC29-5, AND TC97;			
RC	TRANSPOSON-TN5041A1, TN5041B, AND TN5041D1;			
RA	Kholodii G.Y., Gorlenko Z.M., Mindlin S.Z., Nikiforov V.G.;			
RT	*Distribution of distinct microvariants of Tn5041 in environmental bacteria.*			
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AJ422128; CAD19527.1; -			
DR	EMBL; AJ422129; CAD19528.1; -			
DR	EMBL; AJ422130; CAD19529.1; -			
FT	NON_TER			
SQ	SEQUENCE	10 AA; 1206 MW; 23C47E7401F5A417 CRC64;		

Alignment Scores:
Pred. No.: 2.21e+04 Length: 10
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.87% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x Q8RJF1 (1-10)

Qy 454 CCCAGGACCCATCGACCA 437

Db 3 ProArgSerHisArgPro 8

RESULT 2

Q26092 Q26092 PRELIMINARY; PRT; 11 AA.

AC Q26092;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Sea STAR histone H2B gene 5' region (fragment).
OS Pisaster ochraceus (Sea star).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC Asteroidea; Forcipulatacea; Forcipulatida; Asteroidea; Pisaster.
OX NCBI_TaxID=7612;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPERM;
RA Howell A.M., Cool D., Hewitt J., Ydenberg B., Smith M.J., Honda B.M.;
RT "Organization and Unusual Expression of Histone Genes in the Sea Star
RT Pisaster ochraceus";
RL J. Mol. Evol. 25:29-36(1987).
DR EMBL; X05619; CAA29106.1; -;
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1128 MW; 5173974A3865BDD3 CRC64;

Alignment Scores:
Pred. No.: 2.18e+04 Length: 11
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.87% Indels: 0
DB: 5 Gaps: 0

US-09-824-647-16 (1-2095) x Q26092 (1-11)

Qy 278 GCCTCTGGGAAGGGCAG 261

Db 5 AlaSerGlyLysGlyGln 10

RESULT 3

Q08979 Q08979 PRELIMINARY; PRT; 9 AA.

AC Q08979;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE AML1 protein (fragment).
GN AML1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=NMRI; TISSUE=MURINE RETROVIRUS INDUCED TUMOR;
RX MEDLINE=97332339; PubMed=9188573;
RA Antoft H.W., Sorensen A.B., Bareil C., Schmidt J., Luz A.,
RA Pedersen F.S.;
RT "Stability of AML1 (core) site enhancer mutations in T-lymphomas
induced by attenuated SL3-3 murine leukemia virus mutants.";

RL J. Virol. 71:5080-5087(1997).
DR EMBL; Y11802; CAA72496.1; -;
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 981 MW; 293E01E865A776D8 CRC64;

Alignment Scores:

Pred. No.: 4.58e+07 Length: 9
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.73% Indels: 0
DB: 11 Gaps: 0

US-09-824-647-16 (1-2095) x Q08979 (1-9)

Qy 565 CCATCAGGCGACCGG 651

Db 4 ProSerGlyHisArg 8

RESULT 4

P83056 P83056 PRELIMINARY; PRT; 9 AA.

AC P83056;
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Bradykinin-like peptide ([Ala3,Thr6]bradykinin).
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;

RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.

RC TISSUE=SKIN SECRETION;
RA Chen T.B., Orr D.F., Bjourson A.J., McClean S., Rao P.F., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens.";
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- TISSUE SPECIFICITY: SKIN.
SQ SEQUENCE 9 AA; 1048 MW; 3393D771A9C87DC7 CRC64;

Alignment Scores:

Pred. No.: 4.58e+07 Length: 9
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 13 Gaps: 0

US-09-824-647-16 (1-2095) x P83056 (1-9)

Qy 979 CCCGGGGGTTTACG 993

Db 2 ProAlaGlyPheThr 6

RESULT 5

P82923 P82923 PRELIMINARY; PRT; 10 AA.

AC P82923;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Mitochondrial 28S ribosomal protein S2 (MRP-S2) (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=LIVER;
RA Koc E.C., Burkhart W., Blackburn K., Moseley A., Spremulli L.L.;

RT *Small subunit of the mammalian mitochondrial ribosome. Identification
 of the full complement ribosomal proteins present.*;
 RL Submitted (DEC-2000) to the SWISS-PROT data bank.

CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
 CC -1- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro: IPR001865; Ribosomal_S2.
 DR Pfam: PF00318; Ribosomal_S2; PARTIAL.
 DR PRINTS: PR00395; Ribosomal_S2; PARTIAL.
 DR PROSITE: PS00962; RIBOSOMAL_S2.1; PARTIAL.
 KW Ribosomal protein; Mitochondrion.
 FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1246 MW; 6A7A6679C04B476B CRC64;

Alignment Scores:
 Pred. No.: 2.21e+05 Length: 10
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.73% Indels: 0
 DB: 6 Gaps: 0

US-09-824-647-16 (1-2095) x P82923 (1-10)

QY 358 ATCTTGGAGCAGG 344
 DB 6 IlePheGlySerArg 10

RESULT 6

Q9TRU6 PRELIMINARY; PRT; 10 AA.

ID Q9TRU6
 AC Q9TRU6
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE GAP-3, GTPase-activating protein (fragment).
 OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]

RP SEQUENCE.

RX MEDLINE-92112868; PubMed-1309786;

RA Nice E.C., Fabri L., Hammacher A., Holden J., Simpson R.J.,

RA Burgess A.W.;

RT *The purification of a Rap1 GTPase-activating protein from bovine

RT brain cytosol.*;
 RL J. Biol. Chem. 267:1546-1553(1992).

FT NON_TER 1 1

FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1149 MW; 59370A51A72321A7 CRC64;

Alignment Scores:

Pred. No.: 2.21e+05 Length: 10
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.72% Indels: 0
 DB: 6 Gaps: 0

US-09-824-647-16 (1-2095) x Q9TRU6 (1-10)

QY 820 CTCCTCACTAAGCTG 834

DB 2 LeuLeuThrLysLeu 6

RESULT 7

Q9T2P3 PRELIMINARY; PRT; 10 AA.

ID Q9T2P3

AC Q9T2P3

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Cytochrome P-450 27/25-HYDROXYLASE-52 kDa isoform (Fragment).
 OS Rattus sp.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-91355184; PubMed-1883820;
 RA Addya S., Zheng Y.M., Shayiq R.M., Fan J.Y., Avadhani N.G.;
 RT *Characterization of a female-specific hepatic mitochondrial
 cytochrome P-450 whose steady-state level is modulated by
 testosterone.*;
 RL Biochemistry 30:8323-8330(1991).
 FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1092 MW; 316CFB4072DDDC7 CRC64;

Alignment Scores:

Pred. No.: 2.21e+05 Length: 10
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.72% Indels: 0
 DB: 8 Gaps: 0

US-09-824-647-16 (1-2095) x Q9T2P3 (1-10)

QY 890 GCTATACCTGCTGCC 904

DB 1 AlaileProAlaala 5

RESULT 8

Q8SHP0 PRELIMINARY; PRT; 10 AA.

ID Q8SHP0

AC Q8SHP0

DT 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Cytochrome c oxidase subunit I (Fragment).

COI.

OS Bradypodion adolfi.

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae;

OC Bradypodion.

OX NCBI_TaxID=179885;

RN [1]

RP SEQUENCE FROM N.A.

RA Townsend T.M., Larson A.L.;

RT *Molecular Phylogenetics and Mitochondrial Genomic Evolution in the

Chamaeleonidae (Reptilia, Squamata).*

RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF448727; AAL90463.1;

KW Mitochondrion.

FT NON_TER 10 10

SQ SEQUENCE 10 AA; 1303 MW; 5E218E2733641767 CRC64;

Alignment Scores:

Pred. No.: 2.21e+05 Length: 10
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.72% Indels: 0
 DB: 8 Gaps: 0

US-09-824-647-16 (1-2095) x Q8SHP0 (1-10)

QY 879 CTGCCAGATGGCTA 893

DB 3 LeuProArgTrpLeu 7

RESULT 9

Q8SHM2 PRELIMINARY; PRT; 10 AA.
 AC Q8SHM2; 10 AA.
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Calumma boettgeri.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Calumma.
 OX NCBI_TaxID=179899;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Townsend T.M., Larson A.L.;
 RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
 Chamaeleonidae (Reptilia, Squamata).";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF448733; AAL90481.1;
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1303 MW; 5E218E2733641767 CRC64;
 Alignment Scores:
 Pred. No.: 2.21e+05 Length: 10
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.72% Indels: 0
 DB: 8 Gaps: 0

US-09-824-647-16 (1-2095) x Q8SHM2 (1-10)

QY 879 CTGCCAGATGGCTA 893
 Db 3 LeuProArgTripleu 7

RESULT 10

Q8SHL3 PRELIMINARY; PRT; 10 AA.
 AC Q8SHL3; 10 AA.
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Calumma furcifer.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Calumma.
 OX NCBI_TaxID=179902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Townsend T.M., Larson A.L.;
 RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
 Chamaeleonidae (Reptilia, Squamata).";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF448736; AAL90490.1;
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1303 MW; 5E218E2733641767 CRC64;
 Alignment Scores:
 Pred. No.: 2.21e+05 Length: 10
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.72% Indels: 0
 DB: 8 Gaps: 0

US-09-824-647-16 (1-2095) x Q8SHL3 (1-10)

QY 879 CTGCCAGATGGCTA 893
 Db 3 LeuProArgTripleu 7

RESULT 11

Q8SHL0 PRELIMINARY; PRT; 10 AA.
 AC Q8SHL0; 10 AA.
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Calumma gastrotaenia.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Calumma.
 OX NCBI_TaxID=179903;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Townsend T.M., Larson A.L.;
 RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
 Chamaeleonidae (Reptilia, Squamata).";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF448737; AAL90493.1;
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1303 MW; 5E218E2733641767 CRC64;
 Alignment Scores:
 Pred. No.: 2.21e+05 Length: 10
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.72% Indels: 0
 DB: 8 Gaps: 0

US-09-824-647-16 (1-2095) x Q8SHL0 (1-10)

QY 879 CTGCCAGATGGCTA 893
 Db 3 LeuProArgTripleu 7

RESULT 12

Q8SHK1 PRELIMINARY; PRT; 10 AA.
 AC Q8SHK1; 10 AA.
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Calumma nasuta.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Calumma.
 OX NCBI_TaxID=179905;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Townsend T.M., Larson A.L.;
 RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
 Chamaeleonidae (Reptilia, Squamata).";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF448740; AAL90502.1;
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1303 MW; 5E218E2733641767 CRC64;
 Alignment Scores:
 Pred. No.: 2.21e+05 Length: 10
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0

Pred. No.: 2.21e+05 Length: 10
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.73% Indels: 0
 DB: 12 Gaps: 0

US-09-824-647-16 (1-2095) x O90347 (1-10)

QY 341 CGCCGCTGCTGCTG 327
 DB 3 ArgProSerAlaLeu 7

RESULT 17

O60614 PRELIMINARY; PRT; 11 AA.
 AC O60614;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MTG8 related protein (Fragment).
 GN MTG8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE=99009318; PubMed=9790752;
 RA Calabi F., Cilli V.;
 RT "CBFA2T1, a gene rearranged in human leukemia, is a member of a
 multigene family.";
 RL Genomics 52:332-341(1998).
 DR EMBL; AF052211; AAC64700.1;
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1047 MW; CF001CE4DDDB6772 CRC64;

Alignment Scores:
 Pred. No.: 2.19e+05 Length: 11
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.72% Indels: 0
 DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x O60614 (1-11)

QY 920 CCTGGGCGCTGCTG 934
 DB 5 ProGlyAlaAlaLeu 9

RESULT 18

Q9NY38 PRELIMINARY; PRT; 11 AA.
 AC Q9NY38;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE Heavy metal-responsive transcription factor (Fragment).
 GN MTF-1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Auf der Maur A., Belser T., Wang Y., Gunes C., Lichtlen P.,
 RA Georgiev O., Schaffner W.;
 RT "Characterization of the mouse gene for the heavy metal-responsive
 transcription factor MTF-1.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ251881; CAB71327.1; -

FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1099 MW; A8653693773772C6 CRC64;

Alignment Scores:
 Pred. No.: 2.19e+05 Length: 11
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.73% Indels: 0
 DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x Q9NY38 (1-11)

QY 277 CCTCTGGGAGGGGC 263
 DB 6 ProLeuGlyArgGly 10

RESULT 19

Q15997 PRELIMINARY; PRT; 11 AA.
 AC Q15997;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RARA protein (Fragment).
 GN RARA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93222087; PubMed=7682097;
 RA Dong S., Geng J.P., Tong J.H., Wu Y., Cai J.R., Sun G.L., Chen S.R.,
 RA Wang Z.Y., Larsen C.J., Berger R., et al;
 RT "Breakpoint clusters of the PML gene in acute promyelocytic leukemia:
 primary structure of the reciprocal products of the PML-RARA gene in a
 patient with t(15;17).";
 RL Genes Chromosomes Cancer 6:133-139(1993).
 DR EMBL; S57794; AAD13888.1;
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1277 MW; 33C70E22CDDDC417 CRC64;

Alignment Scores:
 Pred. No.: 2.19e+05 Length: 11
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.73% Indels: 0
 DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x Q15997 (1-11)

QY 1461 CGGGCAGCAGCTGCTG 1447
 DB 5 ArgAlaAlaValLeu 9

RESULT 20

O65901 PRELIMINARY; PRT; 11 AA.
 AC O65901;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 DE Phosphoglucose isomerase (Fragment).
 GN PGIC.
 OS Leavenworthia crassa.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euronsids II; Brassicales; Brassicaceae; Leavenworthia.
 OX NCBI_TaxID=70805;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-CV. CR8919/CR15, AND CV. CR8919/CD6;
 RA Liu F., Charlesworth D., Kreitman M.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF054493; AAC19033.1;
 DR EMBL: AF054492; AAC19032.1;
 KW Isomerase.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1208 MW; 5026B3A4BDD87337 CRC64;
 Alignment Scores:
 Pred. No.: 2.19e+05 Length: 11
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.73% Indels: 0
 DB: 10 Gaps: 0
 US-09-824-647-16 (1-2095) x 065901 (1-11)
 QY 1766 CTCAGGCGGCTCC 1752
 Db 4 LeuylsGlyAlaSer 8
 RESULT 21
 O54226 PRELIMINARY; PRT; 12 AA.
 ID O54226
 AC O54226;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE Polyketide synthase (Fragment).
 GN ERYA.
 OS Saccharopolyspora erythraea (Streptomyces erythraeus).
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Pseudonocardiaceae; Pseudonocardiaceae;
 OC Saccharopolyspora.
 OX NCBI_TaxID=1836;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NRRL2338;
 RA Salah-Bey K., Dounith M., Michel J.M., Haydock S., Cortes J.,
 RA Leadlay P.F., Raynal M.C.;
 RT "Targeted gene inactivation for the elucidation of deoxysugar
 RT biosynthesis in the erythromycin producer saccharopolyspora
 RT erythraea";
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Y14332; CAA74712.1;
 FT NON_TER 1 1
 SQ SEQUENCE 12 AA; 1282 MW; D4BA3E57E277337D CRC64;
 Alignment Scores:
 Pred. No.: 2.17e+05 Length: 12
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.73% Indels: 0
 DB: 2 Gaps: 0
 US-09-824-647-16 (1-2095) x O54226 (1-12)
 QY 1881 TGGTTAGGGGAGGT 1867
 Db 6 trpLeuGlyglygly 10
 RESULT 22
 Q9BZ49 PRELIMINARY; PRT; 12 AA.
 ID Q9BZ49
 AC Q9BZ49;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE Glycophorin C (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Patel S.S., Mehlotra R.K., Kastens W., Mgone C.S., Kazura J.W.,
 RA Zimmerman P.A.;
 RT "The association of the glycophorin C exon 3 deletion with
 RT ovalocytosis and malaria susceptibility in the Wosera, Papua New
 RT Guinea";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF342984; AAK01459.1;
 FT NON_TER 1 1
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1361 MW; 2A07044DB837378 CRC64;
 Alignment Scores:
 Pred. No.: 2.17e+05 Length: 12
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.73% Indels: 0
 DB: 4 Gaps: 0
 US-09-824-647-16 (1-2095) x Q9BZ49 (1-12)
 QY 183 GGGTGGCCCTGCCA 197
 Db 5 GlyTrpProLeuPro 9
 RESULT 23
 Q13695 PRELIMINARY; PRT; 12 AA.
 ID Q13695
 AC Q13695;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Acetylcholine receptor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=THYMUS;
 RX MEDLINE=94071933; PubMed=8250918;
 RA Mihovilovic M., Mai Y., Herbstreich M., Rubboli F., Tarroni P.,
 RA Clementi F., Roses A.D.;
 RT "Splicing of an anti-sense Alu sequence generates a coding sequence
 RT variant for the alpha-3 subunit of a neuronal acetylcholine
 RT receptor";
 RL Biochem. Biophys. Res. Commun. 197:137-144(1993).
 DR EMBL: L18973; AAA86792.1;
 KW Receptor.
 FT NON_TER 1 1
 SQ SEQUENCE 12 AA; 1282 MW; 8B0B423A5FC1B2D5 CRC64;
 Alignment Scores:
 Pred. No.: 2.17e+05 Length: 12
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.73% Indels: 0
 DB: 4 Gaps: 0
 US-09-824-647-16 (1-2095) x Q13695 (1-12)
 QY 1904 CAGATGGGTCAG 1890
 Db 8 GlnAsnGlyValGln 12

RESULT 24

Q9UC37 PRELIMINARY; PRT; 12 AA.
 ID Q9UC37
 AC Q9UC37
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Alpha B crystallin fragment 5 (fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92218434; PubMed=1560006;
 RA Kato K., Shinohara H., Goto S., Inaguma Y., Morishita R., Asano T.;
 RT "Copurification of small heat shock protein with alpha B crystallin
 from human skeletal muscle.";
 RL J. Biol. Chem. 267:7718-7725(1992).
 FT NON_TER 1
 FT NON_TER 12
 SQ SEQUENCE 12 AA; 1268 MW; D37BD529CC1B2CD CRC64;

Alignment Scores:

Pred. No.: 2.17e+05 Length: 12
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.72% Indels: 0
 DB: 4 Gaps: 0

US-09-824-647-16 (1-2095) x Q9UC37 (1-12)

QY 746 ACTGCTGCCCCCAAG 760

DB 7 ThrAlaAlaProLys 11
 |||||

RESULT 25

Q93X21 PRELIMINARY; PRT; 12 AA.
 ID Q93X21
 AC Q93X21
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Polyubiquitin homolog (fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. INRA 258; TISSUE=LEAF;
 RX MEDLINE=96236829; PubMed=8680303;
 RA Didierjean L., Frendo P., Nasser W., Genot G., Marivet J., Burkard G.;
 RT "Heavy-metal-responsive genes in maize: identification and comparison
 of their expression upon various forms of abiotic stress.";
 RL Planta 199:1-8(1996).
 DR EMBL; S82313; AAB47175.1;
 FT NON_TER 1
 FT NON_TER 12
 SQ SEQUENCE 12 AA; 1277 MW; 250D2D2F6F340DD8 CRC64;

Alignment Scores:

Pred. No.: 2.17e+05 Length: 12
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.72% Indels: 0
 DB: 10 Gaps: 0

US-09-824-647-16 (1-2095) x Q93X21 (1-12)

QY 561 CACCCACCCCTGGC 575

DB 1 HisProProGly 5
 |||||

RESULT 26

Q93WF2 PRELIMINARY; PRT; 12 AA.
 ID Q93WF2
 AC Q93WF2
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Early nodulin.
 GN ENOD40B.
 OS Lupinus luteus (Yellow lupine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae; Lupinus.
 OX NCBI_TaxID=3873;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. VENTUS;
 RA Podkowiński J., Grabowska B., Kisiel A., Dlugaszewska B.,
 RA Nimmagadda G.;
 RT "ENOD40B from Lupinus luteus.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF352375; AAK51422.1;
 DR EMBL; AF352372; AAK51419.1;
 SQ SEQUENCE 12 AA; 1403 MW; 283958AE7CB326C3 CRC64;

Alignment Scores:

Pred. No.: 2.17e+05 Length: 12
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.73% Indels: 0
 DB: 10 Gaps: 0

US-09-824-647-16 (1-2095) x Q93WF2 (1-12)

QY 1601 TTATCATGGCAGAG 1587

DB 3 LeuSerTrpGlnLys 7
 |||||

RESULT 27

Q69232 PRELIMINARY; PRT; 12 AA.
 ID Q69232
 AC Q69232
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Herpesvirus saimiri gene 7 homologue (fragment).
 OS Bovine herpesvirus 4.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae.
 OX NCBI_TaxID=10385;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=V.TEST;
 RX MEDLINE=92391082; PubMed=1325698;
 RA Bublot M., Lomonte P., Lequarre A.-S., Albrecht J.-C., Nicholas J.,
 RA Fleckenstein B., Pastoret P.-P., Thiry E.;
 RT "Genetic relationships between bovine herpesvirus 4 and the
 gammaherpesviruses Epstein-Barr virus and herpesvirus saimiri.";
 RL Virology 190:654-665(1992).
 DR EMBL; M90772; AAA46019.1;
 FT NON_TER 12
 FT NON_TER 12
 SQ SEQUENCE 12 AA; 1338 MW; 4B800FF17BCDDDD7 CRC64;

Alignment Scores:

Pred. No.: 2.17e+05 Length: 12
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.72% Indels: 0

DB: 12 Gaps: 0

US-09-824-647-16 (1-2095) x Q69232 (1-12)

QY 899 GCTGCGTCTACAGT 913

Db 6 AlaalaValtyrSer 10

RESULT 28

Q69232 ID Q69232 PRELIMINARY; PRT; 12 AA.

AC Q69232; 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Herpesvirus salmieri gene 7 homologue (Fragment).
 OS Bovine herpesvirus 4.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae.
 OX NCBI_TaxID=10385;

[1]

SEQUENCE FROM N.A.

RP STRAIN-V.TEST;

RX MEDLINE-92391082; PubMed-1325698;

RA Bublot M., Lomonte P., Lequarre A.-S., Albrecht J.-C., Nicholas J.,

RA Fleckenstein B., Pastoret P.-P., Thiry E.;

RT "Genetic relationships between bovine herpesvirus 4 and the

RL gammaherpesviruses Epstein-Barr virus and herpesvirus salmieri.,"

RL Virology 130:654-665(1992).

DR EMBL; M30772; AAA46019.1; -

FT NON_TER 12 12

SQ SEQUENCE 12 AA; 1338 MW; 4B800FF17BCDDDD7 CRC64;

Alignment Scores:

Pred. No.: 2.17e+05 Length: 12
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.73% Indels: 0
 DB: 12 Gaps: 0

US-09-824-647-16 (1-2095) x Q69232 (1-12)

QY 1158 CGTGAGTGGCAGCA 1144

Db 3 ArggluLeuAlaala 7

RESULT 29

Q91XP1 ID Q91XP1 PRELIMINARY; PRT; 13 AA.

AC Q91XP1; 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Gamma-glutamyl hydrolase variant II (Fragment).
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

[1]

SEQUENCE FROM N.A.

RP STRAIN-129/SVJ; TISSUE-SPLEEN;

RX MEDLINE-98434456; PubMed-9756990;

RA Esaki T., Roy K., Yao R., Galivan J., Sirotnak F.M.;

RT "Cloning of mouse gamma-glutamyl hydrolase in the form of two cDNA

RT variants with different 5' ends and encoding alternate leader peptide

sequences.,"

RL Gene 219:37-44(1998).

[2]

SEQUENCE FROM N.A.

RP STRAIN-129/SVJ; TISSUE-SPLEEN;

RX MEDLINE-21261955; PubMed-11368914;

RA Masumoto N., Esaki T., Sirotnak F.M.;

RT "Additional organizational features of the murine gamma-glutamyl
 RT hydrolase gene. Two remotely situated exons within the complement C3
 RT gene locus encode an alternate 5' end and proximal ORF under the
 RT control of a bidirectional promoter.,"

RL Gene 268:183-194(2001).

DR EMBL; AF367375; AAK58013.1; -

KW Hydrolase;

FT NON_TER 13 13

SQ SEQUENCE 13 AA; 1544 MW; 7EDA4BEA194E2734 CRC64;

Alignment Scores:

Pred. No.: 2.15e+05 Length: 13
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.72% Indels: 0
 DB: 11 Gaps: 0

US-09-824-647-16 (1-2095) x Q91XP1 (1-13)

QY 447 CTCCTGGGGTGCTG 461

Db 7 LeuLeuGlyValLeu 11

RESULT 30

Q9EIV4

ID Q9EIV4 PRELIMINARY; PRT; 13 AA.

AC Q9EIV4; 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE X protein (Fragment).

GN X.

OS Hepatitis B virus.

OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

OX NCBI_TaxID=10407;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN-2F-1;

RA Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.;

RT "Sequence variation of Hepatitis B virus promoter regions in

RT persistently infected patients.,"

RL Arch. Virol. 146:279-292(2001).

DR EMBL; AF276519; AAG29986.1; -

DR InterPro; IPR000236; TransactX.

DR Pfam; PF00739; X; 1.

FT NON_TER 13 13

SQ SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;

Alignment Scores:

Pred. No.: 2.15e+05 Length: 13
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.72% Indels: 0
 DB: 12 Gaps: 0

US-09-824-647-16 (1-2095) x Q9EIV4 (1-13)

QY 1487 CTCGATCCTCGGAGA 1501

Db 9 LeuaspProAlaarg 13

RESULT 31

Q9EIV3

ID Q9EIV3 PRELIMINARY; PRT; 13 AA.

AC Q9EIV3; 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE X protein (Fragment).

GN X.

OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2F-2;
RX MEDLINE=21213459; PubMed=11315638;
RA Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.;
RT "Sequence variation of Hepatitis B virus promoter regions in
permanently infected patients.";
RL Arch. Virol. 146:279-292(2001).
DR EMBL; AF276520; AAG29987.1; -;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;

Alignment Scores:
Pred. No.: 2.15e+05 Length: 13
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 12 Gaps: 0

US-09-824-647-16 (1-2095) x Q9EIV3 (1-13)

Qy 1487 CTCGATCTCGGAGA 1501
Db 9 LeuAspProAlaArg 13
|||||

RESULT 32

Q9EIV2
ID Q9EIV2 PRELIMINARY; PRT; 13 AA.
AC Q9EIV2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2F-3;
RX MEDLINE=21213459; PubMed=11315638;
RA Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.;
RT "Sequence variation of Hepatitis B virus promoter regions in
permanently infected patients.";
RL Arch. Virol. 146:279-292(2001).
DR EMBL; AF276521; AAG29988.1; -;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;

Alignment Scores:
Pred. No.: 2.15e+05 Length: 13
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 12 Gaps: 0

US-09-824-647-16 (1-2095) x Q9EIV2 (1-13)

Qy 1487 CTCGATCTCGGAGA 1501
Db 9 LeuAspProAlaArg 13
|||||

RESULT 33

Q9EIV0

ID Q9EIV0 PRELIMINARY; PRT; 13 AA.
AC Q9EIV0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2F-5;
RX MEDLINE=21213459; PubMed=11315638;
RA Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.;
RT "Sequence variation of Hepatitis B virus promoter regions in
permanently infected patients.";
RL Arch. Virol. 146:279-292(2001).
DR EMBL; AF276523; AAG29990.1; -;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;

Alignment Scores:
Pred. No.: 2.15e+05 Length: 13
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 12 Gaps: 0

US-09-824-647-16 (1-2095) x Q9EIV0 (1-13)

Qy 1487 CTCGATCTCGGAGA 1501
Db 9 LeuAspProAlaArg 13
|||||

RESULT 34

Q9EIV0
ID Q9EIV0 PRELIMINARY; PRT; 13 AA.
AC Q9EIV0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2F-6;
RX MEDLINE=21213459; PubMed=11315638;
RA Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.;
RT "Sequence variation of Hepatitis B virus promoter regions in
permanently infected patients.";
RL Arch. Virol. 146:279-292(2001).
DR EMBL; AF276524; AAG29991.1; -;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;

Alignment Scores:
Pred. No.: 2.15e+05 Length: 13
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 12 Gaps: 0

US-09-824-647-16 (1-2095) x Q9EIV0 (1-13)

QY 1487 CTCGATCCTCGGAGA 1501
 DB 9 LeuAspProAlaArg 13

RESULT 35
 Q9E1U8 PRELIMINARY; PRT; 13 AA.
 ID Q9E1U8
 AC Q9E1U8; 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE x protein (Fragment).
 GN x.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2F-7;
 RX MEDLINE=21213459; PubMed=11315638;
 RA Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.;
 RT "Sequence variation of Hepatitis B virus promoter regions in
 RT persistently infected patients.";
 RL Arch. Virol. 146:279-282(2001).
 DR EMBL; AF276525; AAG29992.1; -;
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;

Alignment Scores:
 Pred. No.: 2.15e+05 Length: 13
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.72% Indels: 0
 DB: 12 Gaps: 0

US-09-824-647-16 (1-2095) x Q9E1U8 (1-13)

QY 1487 CTCGATCCTCGGAGA 1501
 DB 9 LeuAspProAlaArg 13

RESULT 36
 Q9E1U6 PRELIMINARY; PRT; 13 AA.
 ID Q9E1U6
 AC Q9E1U6; 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE x protein (Fragment).
 GN x.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=4F-9;
 RX MEDLINE=21213459; PubMed=11315638;
 RA Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.;
 RT "Sequence variation of Hepatitis B virus promoter regions in
 RT persistently infected patients.";
 RL Arch. Virol. 146:279-292(2001).
 DR EMBL; AF276527; AAG29994.1; -;
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;

Alignment Scores:
 Pred. No.: 2.15e+05 Length: 13
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.72% Indels: 0
 DB: 12 Gaps: 0

Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.72% Indels: 0
 DB: 12 Gaps: 0

US-09-824-647-16 (1-2095) x Q9E1U6 (1-13)

QY 1487 CTCGATCCTCGGAGA 1501
 DB 9 LeuAspProAlaArg 13

RESULT 37
 Q9E1U5 PRELIMINARY; PRT; 13 AA.
 ID Q9E1U5
 AC Q9E1U5; 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE x protein (Fragment).
 GN x.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=4F-7;
 RX MEDLINE=21213459; PubMed=11315638;
 RA Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.;
 RT "Sequence variation of Hepatitis B virus promoter regions in
 RT persistently infected patients.";
 RL Arch. Virol. 146:279-292(2001).
 DR EMBL; AF276528; AAG29995.1; -;
 DR InterPro; IPR000236; TransactX.
 DR Pfam; PF00739; X; 1.
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;

Alignment Scores:
 Pred. No.: 2.15e+05 Length: 13
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.72% Indels: 0
 DB: 12 Gaps: 0

US-09-824-647-16 (1-2095) x Q9E1U5 (1-13)

QY 1487 CTCGATCCTCGGAGA 1501
 DB 9 LeuAspProAlaArg 13

RESULT 38
 Q9E1U4 PRELIMINARY; PRT; 13 AA.
 ID Q9E1U4
 AC Q9E1U4; 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE x protein (Fragment).
 GN x.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=4F-6;
 RX MEDLINE=21213459; PubMed=11315638;
 RA Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.;
 RT "Sequence variation of Hepatitis B virus promoter regions in
 RT persistently infected patients.";
 RL Arch. Virol. 146:279-292(2001).
 DR EMBL; AF276529; AAG29996.1; -;

```
DR InterPro: IPR000236; TransactX.
DR Pfam: PF00739; X; 1. 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;

Alignment Scores:
Pred. No.: 2.15e+05 Length: 13
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 12 Gaps: 0

US-09-824-647-16 (1-2095) x Q9E1U4 (1-13)
QY 1487 CTCGATCCGCGAGA 1501
Db 9 LeuAspProAlaArg 13

RESULT 39
Q9E1U3
ID Q9E1U3 PRELIMINARY; PRT; 13 AA.
AC Q9E1U3;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4F-5;
RX MEDLINE=21213459; PubMed=11315638;
RA Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.;
RT "Sequence variation of Hepatitis B virus promoter regions in
RT persistently infected patients.";
RL Arch. Virol. 146:279-292(2001).
DR EMBL: AF276530; AAG29997.1; -
DR InterPro: IPR000236; TransactX.
DR Pfam: PF00739; X; 1.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;

Alignment Scores:
Pred. No.: 2.15e+05 Length: 13
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 12 Gaps: 0

US-09-824-647-16 (1-2095) x Q9E1U3 (1-13)
QY 1487 CTCGATCCGCGAGA 1501
Db 9 LeuAspProAlaArg 13

RESULT 40
Q9E1U2
ID Q9E1U2 PRELIMINARY; PRT; 13 AA.
AC Q9E1U2;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RC STRAIN=4F-4;
RX MEDLINE=21213459; PubMed=11315638;
RA Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.;
RT "Sequence variation of Hepatitis B virus promoter regions in
RT persistently infected patients.";
RL Arch. Virol. 146:279-292(2001).
DR EMBL: AF276531; AAG29998.1; -
DR InterPro: IPR000236; TransactX.
DR Pfam: PF00739; X; 1.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;

Alignment Scores:
Pred. No.: 2.15e+05 Length: 13
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 12 Gaps: 0

US-09-824-647-16 (1-2095) x Q9E1U2 (1-13)
QY 1487 CTCGATCCGCGAGA 1501
Db 9 LeuAspProAlaArg 13

RESULT 41
Q9E1U1
ID Q9E1U1 PRELIMINARY; PRT; 13 AA.
AC Q9E1U1;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4F-3;
RX MEDLINE=21213459; PubMed=11315638;
RA Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.;
RT "Sequence variation of Hepatitis B virus promoter regions in
RT persistently infected patients.";
RL Arch. Virol. 146:279-292(2001).
DR EMBL: AF276532; AAG29999.1; -
DR InterPro: IPR000236; TransactX.
DR Pfam: PF00739; X; 1.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;

Alignment Scores:
Pred. No.: 2.15e+05 Length: 13
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 12 Gaps: 0

US-09-824-647-16 (1-2095) x Q9E1U1 (1-13)
QY 1487 CTCGATCCGCGAGA 1501
Db 9 LeuAspProAlaArg 13

RESULT 42
Q9E1U0
ID Q9E1U0 PRELIMINARY; PRT; 13 AA.
AC Q9E1U0;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
```

DE X protein (Fragment).

GN Hepatitis B virus.
OS Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4F-2;
RX MEDLINE=21213459; PubMed=11315638;
RA Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.;
RT "Sequence variation of Hepatitis B virus promoter regions in
RT persistently infected patients.";
RL Arch. Virol. 146:279-292(2001).
DR EMBL; AF276533; AAG30000.1; -;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;

Alignment Scores:

Pred. No.: 2.15e+05 Length: 13
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 12 Gaps: 0

US-09-824-647-16 (1-2095) x Q9E1U0 (1-13)

QY 1487 CTCGATCCTCGGAGA 1501

Db 9 LeuAspProAlaArg 13

RESULT 43

Q9E1T9 PRELIMINARY; PRT; 13 AA.
AC Q9E1T9;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4F-11;
RX MEDLINE=21213459; PubMed=11315638;
RA Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.;
RT "Sequence variation of Hepatitis B virus promoter regions in
RT persistently infected patients.";
RL Arch. Virol. 146:279-292(2001).
DR EMBL; AF276534; AAG30001.1; -;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;

Alignment Scores:

Pred. No.: 2.15e+05 Length: 13
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 12 Gaps: 0

US-09-824-647-16 (1-2095) x Q9E1T9 (1-13)

QY 1487 CTCGATCCTCGGAGA 1501

Db 9 LeuAspProAlaArg 13

RESULT 44

Q9E1T8 PRELIMINARY; PRT; 13 AA.
AC Q9E1T8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4F-10;
RX MEDLINE=21213459; PubMed=11315638;
RA Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.;
RT "Sequence variation of Hepatitis B virus promoter regions in
RT persistently infected patients.";
RL Arch. Virol. 146:279-292(2001).
DR EMBL; AF276535; AAG30002.1; -;
DR InterPro; IPR000236; TransactX.
DR Pfam; PF00739; X; 1.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;

Alignment Scores:

Pred. No.: 2.15e+05 Length: 13
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 12 Gaps: 0

US-09-824-647-16 (1-2095) x Q9E1T8 (1-13)

QY 1487 CTCGATCCTCGGAGA 1501

Db 9 LeuAspProAlaArg 13

RESULT 45

Q52840 PRELIMINARY; PRT; 14 AA.
AC Q52840;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE Homology with C-terminus of other Rhizobium nodB genes.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OC NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97002748; PubMed=8850088;
RA Scott D.B., Young C.A., Collins-Emerson J.M., Terzaghi E.A.,
RA Rockman E.S., Lewis P.E., Pankhurst C.E.;
RT "Novel and complex chromosomal arrangement of Rhizobium loti
RT nodulation genes.";
RL Mol. Plant Microbe Interact. 9:187-197(1996).
DR EMBL; L06241; AAB47352.1; -;
SQ SEQUENCE 14 AA; 1600 MW; 90C26EC32C8F34C5 CRC64;

Alignment Scores:

Pred. No.: 2.14e+05 Length: 14
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.72% Indels: 0
DB: 2 Gaps: 0

US-09-824-647-16 (1-2095) x Q52840 (1-14)

Tue Jul 8 07:45:11 2003

us-09-824-647-16.lim.rspt

Page 14

Qy 501 CTGCTGTCGCGACGG 515
|||||
Db 5 LeuLeuSerAlaArg 9

Search completed: July 7, 2003, 16:19:29
Job time : 137.5 secs